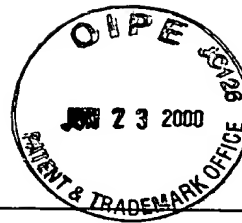


SEQUENCE LISTING



<110> Worley, Paul F.
Lanahan, Anthony

<120> IMMEDIATE EARLY GENES AND METHODS OF USE
THEREFOR

<130> JHU1530-3

<140> 09/245,277

<141> 1999-02-05

<150> 60/074,518

<151> 1998-02-12

<150> 60/074,135

<151> 1998-02-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 527

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(527)

<223> n = A,T,C or G

<400> 1

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acccacacag	aatgccaaagt	tggctggaat	gtaacccaac	ctagttttctg	cgcttcgctc	180
ctctcccagt	gcaagggtgct	aaacacccac	tcacaagcct	gctgtcaagc	tgcgaccttg	240
ggggctgggt	agaaagggct	gcctccttcc	agcaatagaa	gttcatgaat	ttgaggctgg	300
agataggtca	agaccactgt	gataactata	aagactgtag	cagccacaaa	ggagaccccc	360
aaataactgg	aggcatgggc	actgacgtac	cagatgaggt	tatgtttgga	gctgaaggct	420
tgctctgtgc	ttcttggtag	catcttttgt	cctcttgga	catggttgac	cccatactgt	480
ccactgagct	tgggagatga	cagttgaata	aaaaaaaaaa	aaaaaaa		527

<210> 2

<211> 1485

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1485)

<223> n = A,T,C or G

<400> 2

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atgtccttag	gcgaggacat	taactccagt	ctctgacaga	ctttggacat	ccagaataag	180
ttctttttgt	atatcagagc	acagagccca	gcttttagcct	ctgatggacc	tcaggaacca	240

agaaggaggg	acttccttaa	cattctagag	atgggactct	aactctagct	cttgtgttaa	300
gccctgaagt	ccagaaagaa	gtagttcttt	gacattctag	tgccaagatc	cagcctctaa	360
gagaactctg	atgtctaaag	aaagtctttc	atagtctagn	ccagtcacca	gtgaagctaa	420
acacctgaaa	actattagat	tctctggagc	caggaatcca	tctcaagtct	ctcataaagc	480
ccaaatgtcc	caggagaagt	tgacaatata	aagccgtatc	tcgatggact	tttgaagaag	540
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ccatcctttg	atgaaagctc	aaatgtccag	aaagaggggc	ctctctgata	ttctagagta	720
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gaaagagggg	gccttttagaa	caaagactgt	actttttatc	attgataaaag	cacagattcc	1320
agaagcacag	aaatctagaa	agaggggtcct	ccctaacacg	ctcgagctag	aaccccggtg	1380
caagggtctg	aaacttagac	accagaagac	cgctttgtcc	tacaacaagt	ctgcattttc	1440
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<210> 3

<211> 1854

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1854)

<223> r = G or A

y = C or T

m = A or C

k = G or T

s = G or C

w = A or T

<400> 3

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gtagggtccc	attatgtttt	ttttcattag	tggaaactaa	tccttttgtg	ctgtgtttaa	180
tcagtattag	ctttatagaa	ttataaatgt	atattctact	tcttgatcaa	agaacgtagt	240
cgggtattgg	ttttagaagt	tcaaagtgac	actgtatagg	gctttcacgg	ttaatgggat	300
tgttagcaaa	tcttaaggac	atacagccaa	tgattatctg	aggttactgg	ctaactgttt	360
ttcactgagt	tactctgcct	ttttgacatt	tttattcttt	gtttgtcaga	atccagagct	420
tcaggagccc	aaattttttt	atwccgtata	tatatatata	tataaatatc	cataagcctg	480
gtggatttgt	atgcaatgca	ctgcatctat	gtattctgat	agcatctcat	tgatttttgt	540
ttgaaataga	aagaaagata	gtatcccaaa	tgagttatct	ttaacagaaa	gctgagttta	600
acttttatta	cctatataat	aattgatatt	gccaattacc	attctgaatt	tcatatagta	660
taagttagac	attgcttaat	ccccttttaa	atgtattttac	atagacatga	acactcaaat	720
tgctggattt	tttaaataata	tctgacataa	tttttttcat	ctgttacatt	caagttagct	780
tgtttagccc	agatttcaga	atagtaaagg	aggaaaggaa	ccgcattcca	gggaaacctc	840
tgaggccaag	tcagagtcca	gaactgtaaa	cacacaggcc	tgcaagccaa	cattagtcgt	900
gaaatcccta	acacgtcact	ggattctctc	tgtcagcgca	agtgtcagct	gccaaagaat	960
agacttacat	gaagaagtgc	ccacatgctg	gcaggggctg	gccgggtccg	gccagcagac	1020
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tcagtcagca	acctcagaac	tctgaaaaaa	acataaaaaa	gaaaaaaaaa	aaaaaaaam	1140
atgcascctgk	ytacttgtg	aatagtgaat	gtaaaggaaa	gaaaggaaaa	ccaaaagctt	1200
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tgcatttaat	gttaaggaca	gtctgcaata	ataagtaagt	agccagcgtg	ggtgcccagc	1440
agtgttgaga	cctggctgct	ctattgtacg	ctttggaaac	acaatttatg	caacagatgt	1500
ccagatatga	ttctatttat	ggaaaaagtt	tatatgtttt	acaaatgggt	ttaccatctt	1560
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<210> 4
 <211> 1030
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(1030)
 <223> r = G or A
 y = C or T
 m = A or C
 s = G or C
 w = A or T

<400> 4						
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aactaaaatg	gctgtcctgt	gggtttatgc	tggaatatgt	aaccccatca	tcactgtcgt	240
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ccattggttt	tattggcatg	gcggtgcaca	aagctcactc	ttttggcaat	tcattggttac	840
accgtgtggg	cacacaacct	cattgccatt	gctcgtcttc	gtggctyttg	acctaaaagt	900
gctttggaag	tcaccsraag	aaagcattga	ttttgaccaa	ggtgaactag	cccgaaccag	960
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tcttggcacg						1030

<210> 5
 <211> 1824
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(1824)
 <223> r = G or A
 y = C or T
 k = G or T
 s = G or C
 w = A or T
 d = A, G, or T; not C
 n = A, T, C or G

<400> 5

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cttacaattt	gccattcgcc	attcaggctg	cgcaaytggt	gggaagggcn	atcgggtcgg	180
gcctcttcgc	tattacgcca	gctggcgaaa	gggggatgtg	ctgcaaggcg	attaagttgg	240
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gactcactat	agggcggaatt	gggtaccggg	ccccccctcg	aggTCgacgg	tatcgataag	360
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accactgagc	taaatcccca	acccttgtt	ttatTTTTaa	agcaaacgag	atacataatt	480
tcarccatga	taatttaaga	ttatcttgaa	ctcttaagga	aatgtatata	ctaagctatt	540
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atgggggatg	atccgttctc	gtggtgctgc	tggacttatg	cattttggag	gtactgcatg	1440
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aaatatgcag	aaatatcttc	taattcgttg	atcttcgctg	tatgacagtt	ataatattaa	1560
acacttgggt	tgatccactc	tgtttacatt	tatctttcta	agcgtcagaa	agggactaac	1620
ttgaaattat	atctagaggc	tttgtatcat	ttcaaaaatt	aaatttcctt	ggatacttta	1680
ggcaatatct	taaacaactt	tttaataaat	ttaaatat	atatttacgt	aagctaaaat	1740
atacatgaat	gtgcttttta	ataaaattaa	tacagtttat	acttattttgc	caattcacaa	1800
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<210> 6

<211> 1230

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1230)

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m = A or C

s = G or C

w = A or T

<400> 6

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ggtactcaca	acatgttcca	ggaggagmct	ggggccagga	ttttgaccag	agggtatggg	180
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tttcaaagat	cgattgtcgt	tcctgtgggg	acagtggctc	ctaagaaatc	tgcatgttag	480
gagaagacaa	tgaaagacc	tgcccctgtc	tctcaaaact	taactctctg	tatgatttaa	540
aaaaaaattc	catttacttt	acttttgggt	tacttgattt	tgaggaagaa	aatattcaac	600
tttgataaaa	gactaggtat	cagggtttct	tttgcagtgg	gagttgtata	tatatcgtat	660
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gcagtgaat	ttgctattag	accctggagg	caaacgagtt	gtacaagggt	ttatggctcc	780
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ttrtwcwmgt	tttatgtwct	tgttgccttg	ttggctttcc	tactttccac	tgagtagcat	1140
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa				1230

<210> 7

<211> 1516

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1516)

<223> n = A,T,C or G

<400> 7

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caggggaagat	gtgagaagga	tggcctgaca	tcagatgaca	agaggtctta	tagcacatct	300
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<210> 8

<211> 1534

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1534)

<223> n = A,T,C or G

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<210> 14

<211> 953

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(953)

<223> r = A or G

y = C or T

<400> 14

catataaatg	tacttttattg	ttttaaacag	aacgaaagaa	gaggcagaaa	acattttgcat	60
gtaagtcccta	gcttataaat	gtagttttta	gtgggtggcat	ctctaacacg	tcgttcaggg	120
actgttttct	tttgctctct	tgtactgtga	gcactgacac	ttgagaaaag	cacatctggc	180
ggacatatgt	ctccagaact	ggaagaactt	ggagagcaaa	cattttttct	aattcctcta	240
agtaatcttt	agtaaaacaa	aagatgatct	ttggcataga	ttcatacttt	aaaggcattg	300
atatgcattt	atatcaggta	agcaactata	cagatctgct	gagagctttc	aaaagaatct	360
gttatcagct	gaaaggaaat	aggggaagcc	tgagtattca	gggtcaactt	aagatttgca	420
agttcagtg	tggggtcaac	atactagatg	tgggaagaac	atccaggcaa	ggtcttagtc	480
ctgtattcac	ctggttcttg	atttctggaa	gaagcatcca	tgcgctagga	aatgcttata	540
cagccgaggt	aaatgcaaaa	atgagtaaag	tcactttttc	actaactttg	cccaataggr	600
aacatgcctt	tctgataagt	agataccata	ctctttattc	ttgaataact	tatattgaga	660
gaaggttgta	gttggttaaa	agcaactggg	aactataact	tcctactgat	ttttccctag	720
cagcaccaga	attatattct	gcaaatgcta	ttctccctta	cataggaaat	atccttcaga	780
caaaattgcc	tttccattca	gtctcttaag	agyttaat	tgaatggact	tttcaaagtt	840
acaagcaaag	tcaagtgtgg	tggtaggagc	taagaggctg	acacaagtag	atgacttgaa	900
tccagaagtt	caagactagc	ctggacaaca	tagagagacc	cagtctcaaa	att	953

<210> 15

<211> 911

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(911)

<223> n = A, T, C, or G

<400> 15

ggcggggatc	tctcggtctg	taagaagggg	cagtgggtacc	angcgggcac	ttattcagtg	60
tgccaaggat	atcgccaagg	cctctgatga	ggtgacgagg	ttggccaagg	agggttgcaa	120

gcagtgcaca	gataangcgg	nttagaacca	atctcttaca	ggctctgtgag	cgaatcccaa	180
ctataagcac	ccagctcaaa	atcctgtcca	cagtgaaggc	caccatgctg	ggccggacca	240
acatcagtga	cgaggagtct	gagcaggcca	cagagatgct	ggttcataat	gccagaacc	300
tcatgcagtc	tgtgnaagag	actgtgcgag	aggccgaagc	tgcttcaatc	aagattcgan	360
cagacgcgg	atttactctg	cgctgggtca	gaaagactcc	ctgggtaccag	taggcacctg	420
gtcagacctg	gctggtacac	agacctctgc	taatgangan	gtgaccatct	tgagcttcag	480
aagccattca	gagttgccaa	gggggtggnaa	atcaatccct	ggtttcacac	accaagaaag	540
ggaatggggc	ctccttcaca	ttagaataaa	catttatact	cttgtcatgg	gacactttga	600
aagtgtctct	cctacaaaac	ccctgggtacc	tttcaggntt	actccnggtn	gcaanntcct	660
cccccaagg	gaatTTTTTT	ccaataaaa	gctcaaggaa	ttaanggcgn	ttgaaaacca	720
acntnatcca	angggaaang	cccccntggc	cttctggccc	ccttgggggn	acaatttttc	780
ntcccnctgg	gtgtttttaa	tggggtttca	accttggggc	tggncctttt	tccncccccc	840
cttttaagg	gttcctccg	aaggaacctn	agaaaacttn	aagggccaaa	gntccanttt	900
acnaataact	g					911

<210> 16

<211> 621

<212> DNA

<213> Eukaryote

<400> 16

TTTTTTTTTT	TTTTTTTTTC	TCCCTTAAAA	GATAAACTAA	TAAACTCTTC	AATGGTCTTT	60
tcagtatagt	tcttatgtag	tttaacatag	cttataaatt	gagtttaaca	ataaactcaa	120
gaagataatt	ttataaacc	tgTTTTCCAA	tctgtcattt	acttaaatta	TTTTGGTTGT	180
tttccctttt	tttccctctt	tctcaccccc	tccctctcca	tgaagattca	ggTgcttaac	240
atatcatttt	tttccctgct	ggaatttttag	cattgatatg	aaccatggac	aagtatatct	300
tgctgccaca	aagactgtaa	agtgtctcat	ttcaacagct	gaggcaagcc	aagtgatcat	360
taataaaagt	tttcttgctt	ccttcagtgg	tgTTGGTAGT	aaaatggtag	gtaaaagtta	420
ggctgcaagt	tcaataaatg	agattttacct	atcattccac	ccttgtgtat	tcattcacct	480
atcctgggtc	aagcagtttg	agtcaactag	gcatttaaag	gcattgtgtt	tattacttta	540
tggttccaac	tttacatact	tgtcagggat	gaagtctgat	aggTTAAGGA	cagtagaaat	600
ttctgtgcaa	caagcagcaa	c				621

<210> 17

<211> 567

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(567)

<223> n = A, T, C, or G

<400> 17

TTTTTTTTTT	TTTTTGGTTA	CAAAAgtatt	TATTTTATAA	Aacttgtatt	TAAAatagag	60
cttatctgtc	tactcacaaa	tcctaattta	aaacataaca	cattatcctt	agctaactctg	120
atgttaacct	ttacaatcaa	cactcatttt	tgtaatttta	ttagaacctt	gtactaaatg	180
aagtttttta	tcagaaaaca	ttccctttta	tcttaaaaagt	gcttcttaaa	tgaaggcacc	240
aacaagaact	actttcagat	ggtacagaat	ttcttatttc	ttgaagactc	tgtggttgac	300
cacttcttca	ttagttacct	gcagcaagac	accttctctg	caaaggaaaa	aaaaaagtat	360
ctgaagaagt	ttatcatgtt	tgtccaaaga	acctaagtaa	cttcagtggg	ggTTTTtagga	420
ttaaagcaga	ctcactgatg	tgtatacgcc	ctgaatatca	catttctgga	aaggcagtaa	480
agcctagaaa	tcagaaggcg	ggcggtttta	aagaaatttc	aatagccaac	ctacaacant	540
ttagggcaaa	gataatgggc	aaaaant				567

<210> 18

<211> 346

<212> DNA

<213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(346)
 <223> r = A or G
 y = T or C
 m = A or C
 k = G or T
 s = G or C
 w = A or T
 b = G, C, or T; not A
 d = A, G, or T; not C
 h = A, C, or T; not G
 v = A, G, or C; not T
 n = A, T, G, or C

<400> 18
 acgatatmta ywgarrtwya wctstthact gaatmwhatg cacaaatatt aactagtrrt 60
 ttattaaaca gatatsattt agaacaagac ttaawkaaat acaaatcctt aggtacgrtt 120
 taatatcatg ttcadgatgt ttgaagagtt taaaaagaat cactgattaa gkkaagcatc 180
 cbcacttttc tttgagaabc caaacctttt aggnaaadac cccattccaa attttgtccc 240
 chatttcagr cckkcagaaa gtctctaaca tsaagagtc tcaacggggn gtaactcava 300
 wctcetatca agtgcagtaa cctagctctc ccggdggcca tggcgt 346

<210> 19
 <211> 803
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(803)
 <223> n = A, C, T, or G

<400> 19
 aaactaaaca gtgttttgtt aattcttctg cattcggact attgcaggca ttagagcatc 60
 cagagctacg aagggctggc tgcagcagca ccgccctttg taagccagca gaccagcctt 120
 aactgtgggc ttgactcctg tgagctggcc tcagtgtgac tcagaaatgt ttgattagca 180
 gatgagagag cgaggacaca ccacgagggc tgcgttctct tcctccagcg ctgtgcagga 240
 cagtttcttc tcacctagc ctttttaaat gcaccagaag tacagacagt tgcactacac 300
 aaaccctttg aacacttgta gaaatcagtc caccgtagat tagacagaat caccttccaa 360
 tcctttgact tcttttcctt tcatttgaac aattgtataa taattgatta ttgtcaaat 420
 tttgtctgtg gtagtatcgc tttaatttat cttagtacat caacgttttg atttaaaaaa 480
 gaattaaaac aacaaaaaaa gtcacttaga agccatgaac tttttttttt ngatngggaa 540
 attttcttgt ttngaaaatt atcattgggg ttctccgga aancttgtaa gattggntta 600
 taaggtagct gggangttca naacnggtgg ntataccctt ttttaaggga aattaatgat 660
 ttngagtttt tgggccaact ncgggantgg cagggaacc annnggggn ggggtttaaa 720
 ttntgtgagg gttttttggg cctnaatttt ttgcataatt ttcacctngn aacctttnaa 780
 nntnngaaa aaaaaaaaaa cnt 803

<210> 20
 <211> 2540
 <212> DNA
 <213> Eukaryote

<220>
 <221> CDS
 <222> (3)...(2348)

<221> misc_feature
 <222> (1)...(2540)

<223> n = A,T,C or G

<400> 20

tg	cag	ccg	ccc	ttg	gaa	ctg	cat	gtc	agg	aag	cat	ccc	ttt	gtg	tat	47
Gln	Pro	Pro	Leu	Glu	Leu	His	Val	Arg	Lys	His	Pro	Phe	Val	Tyr		
1				5				10						15		
gtc	tgt	gct	ata	tgt	ctc	aag	aaa	ttt	gtc	agc	tca	atc	agg	ctg	cgc	95
Val	Cys	Ala	Ile	Cys	Leu	Lys	Lys	Phe	Val	Ser	Ser	Ile	Arg	Leu	Arg	
				20				25						30		
tcc	cat	atc	cga	gag	gtg	cat	ggg	gcg	gcc	cag	gag	acc	ttg	gtt	ttt	143
Ser	His	Ile	Arg	Glu	Val	His	Gly	Ala	Ala	Gln	Glu	Thr	Leu	Val	Phe	
			35				40						45			
act	agc	tcc	atc	aac	cag	agt	ttc	tgc	ctc	ctg	gag	cct	ggg	gat		191
Thr	Ser	Ser	Ile	Asn	Gln	Ser	Phe	Cys	Leu	Leu	Glu	Pro	Gly	Gly	Asp	
		50				55					60					
atc	cag	cag	gaa	gcc	ttg	gga	aac	cag	cta	tca	ctg	aca	gct	gag	gaa	239
Ile	Gln	Gln	Glu	Ala	Leu	Gly	Asn	Gln	Leu	Ser	Leu	Thr	Ala	Glu	Glu	
	65				70				75							
ttt	gtg	tgt	cca	gaa	att	gat	gta	cgt	aag	ggg	gag	gtt	tgt	cct	ggg	287
Phe	Val	Cys	Pro	Glu	Ile	Asp	Val	Arg	Lys	Gly	Glu	Val	Cys	Pro	Gly	
	80				85				90						95	
gaa	gct	cag	cct	gag	gtg	ggg	ctg	agg	gag	ttg	gag	gcc	cct	gga	gaa	335
Glu	Ala	Gln	Pro	Glu	Val	Gly	Leu	Arg	Glu	Leu	Glu	Ala	Pro	Gly	Glu	
				100				105						110		
gca	tgt	gcc	cca	gcc	gtg	ccc	ttg	gcc	aac	ccc	cag	agt	gtc	agt	gtt	383
Ala	Cys	Ala	Pro	Ala	Val	Pro	Leu	Ala	Asn	Pro	Gln	Ser	Val	Ser	Val	
			115				120						125			
tcc	ctg	tcc	ccc	tgc	aaa	ctg	gaa	acc	act	gtg	gtc	aat	tcc	gac	ctc	431
Ser	Leu	Ser	Pro	Cys	Lys	Leu	Glu	Thr	Thr	Val	Val	Asn	Ser	Asp	Leu	
		130				135						140				
aac	tct	ctt	gga	gtg	gtt	tca	gat	gat	ttt	tta	ctg	aaa	act	gat	acc	479
Asn	Ser	Leu	Gly	Val	Val	Ser	Asp	Asp	Phe	Leu	Leu	Lys	Thr	Asp	Thr	
	145					150					155					
tct	tct	gct	gag	cct	cat	gct	gct	gct	gag	cta	acc	tca	gac	aca	cag	527
Ser	Ser	Ala	Glu	Pro	His	Ala	Ala	Ala	Glu	Leu	Thr	Ser	Asp	Thr	Gln	
	160				165				170						175	
cat	cga	ggc	tca	gcc	cag	act	cag	ggg	gaa	gaa	gtc	aca	ctg	ctg	ctg	575
His	Arg	Gly	Ser	Ala	Gln	Thr	Gln	Gly	Glu	Glu	Val	Thr	Leu	Leu	Leu	
			180					185						190		
gcc	aag	gcc	aaa	agt	act	gga	cca	gac	tca	gag	agt	cct	cca	agt	gga	623
Ala	Lys	Ala	Lys	Ser	Thr	Gly	Pro	Asp	Ser	Glu	Ser	Pro	Pro	Ser	Gly	
			195				200					205				
ggg	cag	aat	gtg	ggg	gct	ctg	cca	gcc	agt	gaa	tct	gac	tct	aac	agg	671
Gly	Gln	Asn	Val	Gly	Ala	Leu	Pro	Ala	Ser	Glu	Ser	Asp	Ser	Asn	Arg	
	210					215						220				
tgt	ctc	agg	gca	aac	cca	gca	gag	acc	tca	gac	ctc	ctt	cct	aca	gtg	719

Cys	Leu	Arg	Ala	Asn	Pro	Ala	Glu	Thr	Ser	Asp	Leu	Leu	Pro	Thr	Val	
225						230					235					
gct	gat	gga	gga	gac	ctc	ggt	gtg	tgc	cag	cct	gac	tct	tgc	acg	tcg	767
Ala	Asp	Gly	Gly	Asp	Leu	Gly	Val	Cys	Gln	Pro	Asp	Ser	Cys	Thr	Ser	
240					245				250						255	
tcc	tct	gag	cac	cac	cct	ggc	agc	aca	gca	ttc	atg	aag	gtc	cta	gac	815
Ser	Ser	Glu	His	His	Pro	Gly	Ser	Thr	Ala	Phe	Met	Lys	Val	Leu	Asp	
				260					265					270		
agt	ctc	cag	aag	aag	cag	atg	aac	acc	agt	ctt	tgc	gag	cgg	atc	cgg	863
Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr	Ser	Leu	Cys	Glu	Arg	Ile	Arg	
			275					280						285		
aag	gtt	tat	gga	gac	ctg	gag	tgt	gaa	tac	tgt	ggc	aaa	ctt	ttt	tgg	911
Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu	Tyr	Cys	Gly	Lys	Leu	Phe	Trp	
		290					295					300				
tac	caa	gtg	cat	ttt	gac	atg	cat	gtc	cgc	acc	cac	acc	cgg	gaa	cat	959
Tyr	Gln	Val	His	Phe	Asp	Met	His	Val	Arg	Thr	His	Thr	Arg	Glu	His	
	305					310					315					
ctg	tat	tat	tgc	tcc	cag	tgt	cac	tac	tct	tcc	atc	acc	aaa	aac	tgc	1007
Leu	Tyr	Tyr	Cys	Ser	Gln	Cys	His	Tyr	Ser	Ser	Ile	Thr	Lys	Asn	Cys	
320					325					330					335	
ctt	aaa	cgc	cat	gta	att	cag	aaa	cac	agt	aac	atc	ttg	ctg	aag	tgt	1055
Leu	Lys	Arg	His	Val	Ile	Gln	Lys	His	Ser	Asn	Ile	Leu	Leu	Lys	Cys	
				340					345					350		
ccc	act	gac	ggc	tgt	gac	tac	tcg	act	cca	gat	aaa	tat	aag	cta	cag	1103
Pro	Thr	Asp	Gly	Cys	Asp	Tyr	Ser	Thr	Pro	Asp	Lys	Tyr	Lys	Leu	Gln	
			355					360						365		
gcc	cac	ctt	aaa	gtt	cac	aca	gag	ctg	gac	aaa	agg	agt	tat	tct	tgt	1151
Ala	His	Leu	Lys	Val	His	Thr	Glu	Leu	Asp	Lys	Arg	Ser	Tyr	Ser	Cys	
		370					375					380				
cct	gta	tgt	gaa	aaa	tct	ttt	tca	gaa	gac	cga	ttg	ata	aag	tca	cat	1199
Pro	Val	Cys	Glu	Lys	Ser	Phe	Ser	Glu	Asp	Arg	Leu	Ile	Lys	Ser	His	
	385					390					395					
atc	aag	act	aat	cat	cca	gag	gtc	tcc	atg	aat	acc	att	tct	gag	gtt	1247
Ile	Lys	Thr	Asn	His	Pro	Glu	Val	Ser	Met	Asn	Thr	Ile	Ser	Glu	Val	
400					405					410					415	
ctt	ggg	aga	aga	gtc	cag	ctc	aaa	ggg	cta	att	gga	aag	cga	gcc	atg	1295
Leu	Gly	Arg	Arg	Val	Gln	Leu	Lys	Gly	Leu	Ile	Gly	Lys	Arg	Ala	Met	
				420					425					430		
aag	tgt	ccg	tat	tgc	gat	ttc	tat	ttc	atg	aag	aat	ggc	tca	gac	ctt	1343
Lys	Cys	Pro	Tyr	Cys	Asp	Phe	Tyr	Phe	Met	Lys	Asn	Gly	Ser	Asp	Leu	
			435					440					445			
cag	cgg	cac	atc	tcn	gct	cac	gag	ggg	gtg	aag	ccc	ttc	aaa	tgt	tct	1391
Gln	Arg	His	Ile	Ser	Ala	His	Glu	Gly	Val	Lys	Pro	Phe	Lys	Cys	Ser	
		450					455					460				
ttg	tgt	gag	tat	gca	act	cgt	agc	aag	agc	aac	ctc	aaa	gct	cat	atg	1439

Leu	Cys	Glu	Tyr	Ala	Thr	Arg	Ser	Lys	Ser	Asn	Leu	Lys	Ala	His	Met	
465						470					475					
aat	cgt	cac	agc	act	gag	aag	act	cac	ctc	tgt	gac	atg	tgt	ggc	aag	1487
Asn	Arg	His	Ser	Thr	Glu	Lys	Thr	His	Leu	Cys	Asp	Met	Cys	Gly	Lys	
480					485					490					495	
aaa	ttc	aaa	tcc	aaa	ggg	aca	tta	aag	agt	cat	aag	ctc	ctt	cac	aca	1535
Lys	Phe	Lys	Ser	Lys	Gly	Thr	Leu	Lys	Ser	His	Lys	Leu	Leu	His	Thr	
				500					505					510		
tct	gat	ggg	aag	caa	ttc	aag	tgc	acg	gtg	tgt	gac	tac	aca	gct	gcc	1583
Ser	Asp	Gly	Lys	Gln	Phe	Lys	Cys	Thr	Val	Cys	Asp	Tyr	Thr	Ala	Ala	
			515					520					525			
cag	aaa	cca	cag	ctg	ctg	cga	cac	atg	gag	cag	gat	gcc	tcc	ttc	aag	1631
Gln	Lys	Pro	Gln	Leu	Leu	Arg	His	Met	Glu	Gln	Asp	Ala	Ser	Phe	Lys	
		530					535					540				
cct	ttc	cgc	tgc	gct	cac	tgt	cat	tat	tca	tgt	aac	atc	tct	gga	tct	1679
Pro	Phe	Arg	Cys	Ala	His	Cys	His	Tyr	Ser	Cys	Asn	Ile	Ser	Gly	Ser	
	545					550					555					
ctg	aaa	cgg	cac	tac	aac	agg	aag	cac	ccc	aac	gag	gag	tat	gcc	aac	1727
Leu	Lys	Arg	His	Tyr	Asn	Arg	Lys	His	Pro	Asn	Glu	Glu	Tyr	Ala	Asn	
560					565					570					575	
gtg	ggc	agc	ggg	gag	ctt	gca	gct	gaa	gcc	ctc	atc	caa	caa	ggg	ggg	1775
Val	Gly	Ser	Gly	Glu	Leu	Ala	Ala	Glu	Ala	Leu	Ile	Gln	Gln	Gly	Gly	
				580					585					590		
ctg	aag	tgt	cct	gtt	tgc	agc	ttt	gtg	tat	gga	acc	aaa	tgg	gag	ttc	1823
Leu	Lys	Cys	Pro	Val	Cys	Ser	Phe	Val	Tyr	Gly	Thr	Lys	Trp	Glu	Phe	
			595					600					605			
aac	aga	cac	ttg	aag	aac	aag	cat	ggc	ttg	aag	cca	gcg	aca	gag	act	1871
Asn	Arg	His	Leu	Lys	Asn	Lys	His	Gly	Leu	Lys	Pro	Ala	Thr	Glu	Thr	
		610					615					620				
ccc	gag	gag	ccc	tcc	acc	cag	tat	ctc	tac	atc	acc	gag	gct	gaa	gat	1919
Pro	Glu	Glu	Pro	Ser	Thr	Gln	Tyr	Leu	Tyr	Ile	Thr	Glu	Ala	Glu	Asp	
		625				630					635					
gtt	cag	ggg	aca	caa	gca	gct	gta	gct	gca	ctt	cag	gac	ctg	cga	tat	1967
Val	Gln	Gly	Thr	Gln	Ala	Ala	Val	Ala	Ala	Leu	Gln	Asp	Leu	Arg	Tyr	
640					645					650					655	
acc	tcc	gag	agt	ggg	gat	cga	ctt	gac	ccc	aca	gct	gtg	aat	atc	ctg	2015
Thr	Ser	Glu	Ser	Gly	Asp	Arg	Leu	Asp	Pro	Thr	Ala	Val	Asn	Ile	Leu	
				660					665					670		
cag	cag	atc	att	gaa	ctg	ggg	tca	gag	act	cac	gat	gct	gct	gcc	gtg	2063
Gln	Gln	Ile	Ile	Glu	Leu	Gly	Ser	Glu	Thr	His	Asp	Ala	Ala	Ala	Val	
			675					680					685			
gcc	tcc	gtg	gtt	gcc	atg	gcg	cct	ggg	aca	gtg	act	gtt	gta	aag	cag	2111
Ala	Ser	Val	Val	Ala	Met	Ala	Pro	Gly	Thr	Val	Thr	Val	Val	Lys	Gln	
		690					695					700				
gtc	acc	gat	gag	gaa	ccc	aat	tcc	aac	cat	aca	gtc	atg	atc	cag	gag	2159

Val	Thr	Asp	Glu	Glu	Pro	Asn	Ser	Asn	His	Thr	Val	Met	Ile	Gln	Glu		
705						710					715						
act	ctg	cag	cag	gcc	tct	gtg	gag	ttg	gcc	gag	cag	cac	cat	ctg	gtg	2207	
Thr	Leu	Gln	Gln	Ala	Ser	Val	Glu	Leu	Ala	Glu	Gln	His	His	Leu	Val		
720					725				730					735			
gtg	tcc	tct	gat	gac	gtg	gag	ggc	att	gag	aca	gtg	aca	gtg	tac	aca	2255	
Val	Ser	Ser	Asp	Asp	Val	Glu	Gly	Ile	Glu	Thr	Val	Thr	Val	Tyr	Thr		
				740					745					750			
cag	ggg	ggg	gag	gcc	tca	gag	ttc	atc	gtg	tac	gtg	caa	gag	gct	gtc	2303	
Gln	Gly	Gly	Glu	Ala	Ser	Glu	Phe	Ile	Val	Tyr	Val	Gln	Glu	Ala	Val		
			755					760					765				
cag	ccc	atg	gag	gag	cag	gtc	ggg	gag	cag	cca	gcc	aca	gaa	ctc		2348	
Gln	Pro	Met	Glu	Glu	Gln	Val	Gly	Glu	Gln	Pro	Ala	Thr	Glu	Leu			
		770					775					780					
tagagaatcc	ctgcctcctt	tgccagccag	cctttgtggg	cctgaagacc	tcctaacc	ccaggtccat	ccttggtctt	tcttgccac	tgcccccaga	taaatttctc	cataactgtc	ctctgtgtgg	tcaaagccag	gagagtatca	tgaagagaga	gagagagaga	gactagtctc
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<210> 21
 <211> 782
 <212> PRT
 <213> Eukaryote

<400> 21

Gln	Pro	Pro	Leu	Glu	Leu	His	Val	Arg	Lys	His	Pro	Phe	Val	Tyr	Val		
1				5					10					15			
Cys	Ala	Ile	Cys	Leu	Lys	Lys	Phe	Val	Ser	Ser	Ile	Arg	Leu	Arg	Ser		
			20					25					30				
His	Ile	Arg	Glu	Val	His	Gly	Ala	Ala	Gln	Glu	Thr	Leu	Val	Phe	Thr		
		35				40					45						
Ser	Ser	Ile	Asn	Gln	Ser	Phe	Cys	Leu	Leu	Glu	Pro	Gly	Gly	Asp	Ile		
	50					55					60						
Gln	Gln	Glu	Ala	Leu	Gly	Asn	Gln	Leu	Ser	Leu	Thr	Ala	Glu	Glu	Phe		
65				70						75				80			
Val	Cys	Pro	Glu	Ile	Asp	Val	Arg	Lys	Gly	Glu	Val	Cys	Pro	Gly	Glu		
			85					90					95				
Ala	Gln	Pro	Glu	Val	Gly	Leu	Arg	Glu	Leu	Glu	Ala	Pro	Gly	Glu	Ala		
		100						105					110				
Cys	Ala	Pro	Ala	Val	Pro	Leu	Ala	Asn	Pro	Gln	Ser	Val	Ser	Val	Ser		
		115						120				125					
Leu	Ser	Pro	Cys	Lys	Leu	Glu	Thr	Thr	Val	Val	Asn	Ser	Asp	Leu	Asn		
	130					135					140						
Ser	Leu	Gly	Val	Val	Ser	Asp	Asp	Phe	Leu	Leu	Lys	Thr	Asp	Thr	Ser		
145					150					155					160		
Ser	Ala	Glu	Pro	His	Ala	Ala	Ala	Glu	Leu	Thr	Ser	Asp	Thr	Gln	His		
			165					170						175			
Arg	Gly	Ser	Ala	Gln	Thr	Gln	Gly	Glu	Val	Thr	Leu	Leu	Leu	Ala			
		180						185					190				
Lys	Ala	Lys	Ser	Thr	Gly	Pro	Asp	Ser	Glu	Ser	Pro	Pro	Ser	Gly	Gly		
		195					200					205					
Gln	Asn	Val	Gly	Ala	Leu	Pro	Ala	Ser	Glu	Ser	Asp	Ser	Asn	Arg	Cys		
	210					215					220						
Leu	Arg	Ala	Asn	Pro	Ala	Glu	Thr	Ser	Asp	Leu	Leu	Pro	Thr	Val	Ala		
225					230					235					240		

Asp Gly Gly Asp Leu Gly Val Cys Gln Pro Asp Ser Cys Thr Ser Ser
 245 250 255
 Ser Glu His His Pro Gly Ser Thr Ala Phe Met Lys Val Leu Asp Ser
 260 265 270
 Leu Gln Lys Lys Gln Met Asn Thr Ser Leu Cys Glu Arg Ile Arg Lys
 275 280 285
 Val Tyr Gly Asp Leu Glu Cys Glu Tyr Cys Gly Lys Leu Phe Trp Tyr
 290 295 300
 Gln Val His Phe Asp Met His Val Arg Thr His Thr Arg Glu His Leu
 305 310 315 320
 Tyr Tyr Cys Ser Gln Cys His Tyr Ser Ser Ile Thr Lys Asn Cys Leu
 325 330 335
 Lys Arg His Val Ile Gln Lys His Ser Asn Ile Leu Leu Lys Cys Pro
 340 345 350
 Thr Asp Gly Cys Asp Tyr Ser Thr Pro Asp Lys Tyr Lys Leu Gln Ala
 355 360 365
 His Leu Lys Val His Thr Glu Leu Asp Lys Arg Ser Tyr Ser Cys Pro
 370 375 380
 Val Cys Glu Lys Ser Phe Ser Glu Asp Arg Leu Ile Lys Ser His Ile
 385 390 395 400
 Lys Thr Asn His Pro Glu Val Ser Met Asn Thr Ile Ser Glu Val Leu
 405 410 415
 Gly Arg Arg Val Gln Leu Lys Gly Leu Ile Gly Lys Arg Ala Met Lys
 420 425 430
 Cys Pro Tyr Cys Asp Phe Tyr Phe Met Lys Asn Gly Ser Asp Leu Gln
 435 440 445
 Arg His Ile Ser Ala His Glu Gly Val Lys Pro Phe Lys Cys Ser Leu
 450 455 460
 Cys Glu Tyr Ala Thr Arg Ser Lys Ser Asn Leu Lys Ala His Met Asn
 465 470 475 480
 Arg His Ser Thr Glu Lys Thr His Leu Cys Asp Met Cys Gly Lys Lys
 485 490 495
 Phe Lys Ser Lys Gly Thr Leu Lys Ser His Lys Leu Leu His Thr Ser
 500 505 510
 Asp Gly Lys Gln Phe Lys Cys Thr Val Cys Asp Tyr Thr Ala Ala Gln
 515 520 525
 Lys Pro Gln Leu Leu Arg His Met Glu Gln Asp Ala Ser Phe Lys Pro
 530 535 540
 Phe Arg Cys Ala His Cys His Tyr Ser Cys Asn Ile Ser Gly Ser Leu
 545 550 555 560
 Lys Arg His Tyr Asn Arg Lys His Pro Asn Glu Glu Tyr Ala Asn Val
 565 570 575
 Gly Ser Gly Glu Leu Ala Ala Glu Ala Leu Ile Gln Gln Gly Gly Leu
 580 585 590
 Lys Cys Pro Val Cys Ser Phe Val Tyr Gly Thr Lys Trp Glu Phe Asn
 595 600 605
 Arg His Leu Lys Asn Lys His Gly Leu Lys Pro Ala Thr Glu Thr Pro
 610 615 620
 Glu Glu Pro Ser Thr Gln Tyr Leu Tyr Ile Thr Glu Ala Glu Asp Val
 625 630 635 640
 Gln Gly Thr Gln Ala Ala Val Ala Ala Leu Gln Asp Leu Arg Tyr Thr
 645 650 655
 Ser Glu Ser Gly Asp Arg Leu Asp Pro Thr Ala Val Asn Ile Leu Gln
 660 665 670
 Gln Ile Ile Glu Leu Gly Ser Glu Thr His Asp Ala Ala Val Ala
 675 680 685
 Ser Val Val Ala Met Ala Pro Gly Thr Val Thr Val Val Lys Gln Val
 690 695 700
 Thr Asp Glu Glu Pro Asn Ser Asn His Thr Val Met Ile Gln Glu Thr
 705 710 715 720

Leu Gln Gln Ala Ser Val Glu Leu Ala Glu Gln His His Leu Val Val
 725 730 735
 Ser Ser Asp Asp Val Glu Gly Ile Glu Thr Val Thr Val Tyr Thr Gln
 740 745 750
 Gly Gly Glu Ala Ser Glu Phe Ile Val Tyr Val Gln Glu Ala Val Gln
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 770 775 780

<210> 22
 <211> 1012
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(1012)
 <223> r = G or A
 y = C or T
 m = A or C
 k = G or T
 s = G or C
 w = A or T

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 attacttatt atactcgtgg aactgagata tttarmsrsm gcttwyyttt ttttttttytt 120
 agtgtaaaat acttaagcgt ttccactatt ggaagaaaag catatatggg tatttttgtat 180
 tgtaacttgt ttaaaaggac agtctttttt aaycttccca cttaaagtct tttaaaatat 240
 gtaatacaat ttgaagcttg tttaaaaata gaattaaatg tcttawatag kgctackggt 300
 ttggaattag aaagtgatca aatacaaaac atttttaaata taagcccaga aaacaaaata 360
 gtgttttaaag ttagtttagt ataaaagaaa tttataagat tttttcttca atataagata 420
 cctcacttga aaataaagaa agcacagcac attaaagtaa ttctcatgag aacaccccat 480
 tagaataatt gctaaatcta ggacaccttt tgagttgtga gtttgtgata catgtagtca 540
 ccattagctt ttctgctgga aggacttccc gtagtaattt taaggcagtg taatagttca 600
 attaccccac agtttctaac ctgggaaggc agtatgtgaa tggtcocctc tgcaactacg 660
 gaaacacatt agctacattg agcataactc gattgataat tttgccagtg catatagttt 720
 tatgattaaa attgctgtgg ttgggttgcac tacacgacac acaaaaactgt cctctacctc 780
 acatgaaata aatattttat atgggttttac taaaaaaatg actcatctat ctgggttactt 840
 agttttacaaa ttttggatta tattttattga aacatgacat actgtgctct tagctttatac 900
 ctcaatcgta ttttgtgctg tttgccattt tcatgccttg tatataactt gtatagattg 960
 gatgatattc ccaataaaca cttttaatkc caawraaaaa aaaaaaaaaa aa 1012

<210> 23
 <211> 1747
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(1747)
 <223> n = A,T,C or G

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 ctctagagg agttttcctg atgaaatgct agtagcacct ccccgacata cagcgggtgg 180
 gtggggcaca ctttgcgtg ctctgatggg acacacaaga agcagttgta atttgtcttt 240
 ctgttttaaga gtgaccatag ctagatatgt gtgtgtgact tcagaaaatt aaaatgcttt 300
 ccgaactttt cctgttaata gaggtgtgaa gtactcattc atgtgcatga ggaaagtggg 360

ttccacggac	gcacaccgct	tcctatgtaa	ctcacaatgc	tctgtacagt	ttttatatgt	420
agtcttacaa	aggtcttatg	aaatttatat	aatggatttt	ttctttttaa	ttataaaaata	480
ctaaatatct	taaagattgt	tttggacttt	tgtatgttta	aatgttatct	taaaacttgc	540
acaaatggac	catgatgact	ctttgatctt	aaaatcagga	atttacagtc	agctaagaaa	600
aatgtggata	ggttaataat	ccacagtggg	agtatctgct	aggagcagga	attgtagatg	660
acatgaattc	cgtgatttga	ggaagggcag	cctctgcact	tttctttgtt	tttgtttttt	720
gcacatgaag	tctgacattt	ttaccatcga	atttcacatt	actagatggg	tggcttgagg	780
tttacctagg	ggaaattctt	agcaactttg	tactttgttg	tttttgttct	gtttggtctc	840
cagcttgacg	agaccctctt	gcctctgtct	cccaagtgtt	gggttggcag	gatgagcccc	900
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ttctgtttca	tgtgtcccga	gctgtctcat	ggtactacat	gcagtgaact	gagatctgcg	1020
ttaaggaata	acttaggaga	aaacggctgt	cactgtcctc	cccgctgtga	gacaccagag	1080
ttatcacacc	tgttatggtc	atactttgtg	ttatgatact	gatgtctaag	gcaatttttc	1140
tactttccaa	aaggggagttt	gtttcctaaa	tatatgtgta	cctaaatgtg	gtttttattct	1200
gctatgttct	ataatttatg	tattgacttt	tgtaacctcc	ttgggagaaa	catgttaagt	1260
ggcacaggga	ccatatatgt	cattttattt	agctctggag	aaggaaacca	caggcgtttg	1320
taaaatagca	ttagcttaga	tgtcagttca	ttgtgcttgg	ctgtgtggga	ggcagactca	1380
aggacttgca	ccattttattt	ttctgacaga	agtgttctgc	ttatgtgctg	cttagtaagt	1440
gtgatttttc	tagtcttgat	gaaacttgcc	tcgtgacatt	gttgagcgta	gtcttcactt	1500
tccagaagat	gaaatgatgt	gccatcattt	tctgtctaaa	cttcctttta	agtaattttt	1560
aatcagctgt	aaatacata	tctcctactg	ttgaaagtaa	ctttaattta	cattgcacca	1620
tatagcttga	aaaccaactt	tgaattctg	tactcctcca	caagtgaact	ccgctaaaat	1680
acccatagga	agcttacttt	gtgcatgcnt	gctttgtgtg	ccggttgccg	tcctaanggt	1740
tgctttg						1747

<210> 24

<211> 571

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(571)

<223> n = A,T,C or G

<400> 24

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taaatgcttt	taaaatatgt	aatacaattt	gaagcttggt	taaaaataga	attaaatgtc	180
ttatatagtg	ctactgtttt	ggaattagaa	agtgatcaaa	tacaaaacat	tttaaaatta	240
agcccagaaa	acaaaatagt	gttttaaagtt	agtttagtat	aaaagaaatt	tatgagattt	300
tttcttcaat	ataagatacc	tcacttgaaa	ataaagaaag	cacagcacat	taaagtaatt	360
ctcatgagaa	caccccatca	gaataattgc	taaatctagg	acaccttttg	agttgtgaag	420
tttgtgatac	atgtagtcac	cattagcttt	tctgctggaa	ggacttcccg	tagtaatttt	480
aaagnagtgt	aataagttca	attanccac	aagtttctaa	nctgggaaag	naantatggt	540
gaatggnccc	ttctgcaact	acgggaacac	a			571

<210> 25

<211> 619

<212> DNA

<213> Eukaryote

<400> 25

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acaagttata	tacaaggcat	gaaaatggca	aacagcacaa	aatacgattg	aggtataagc	120
taagagcaca	gtatgtcatg	tttcaataaa	tataatccaa	aatttgtaaa	ctaagtaacc	180
agatagatga	gtcatttttt	tagtaaaacc	atataaaata	ttatttcat	gtgaggtaga	240
ggacagtttt	gtgtgtcgtg	taatgcaacc	aaccacagca	attttaatca	taaaactata	300
tgcactggca	aaattatcaa	tcgagttatg	ctcaatgtag	ctaagtgtgt	tccgtagttg	360
cagaagggac	cattcacata	ctgccttccc	agggttagaaa	ctgtggggta	attgaactat	420

tacactgcct	taaaattact	acgggaagtc	cttccagcag	aaaagcta	ggtgactaca	480
tgtatcacia	actcacaact	caaaaggtgt	cctagattta	gcaattattc	taatggggtg	540
ttctcatgag	aattacttta	atgtgctgtg	ctttctttat	ttcaagtgag	gtatcttata	600
ttgaagaaaa	aatccataa					619

<210> 26

<211> 2995

<212> DNA

<213> Eukaryote

<220>

<221> CDS

<222> (218) ... (1960)

<400> 26

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accccggggc	ccggacgcga	gtggctgcgg	tgtcctgggc	gagcactgct	agtttaggcc	180
gtctgtcctc	agctgcttgg	aaccctaca	tcccacc	atg gct ggg	ata cag aag	235
				Met Ala Gly Ile Gln Lys		
				1	5	
agg aag ttt	gac cag ctg	gaa gag gac	gac tgc agc	tcc tcc tcc	ttg	283
Arg Lys Phe	Asp Gln Leu	Glu Glu Asp	Asp Cys Ser	Ser Ser Ser	Leu	
	10		15		20	
tcc tct ggc	gat ctc tct	ccc tct cct	ccc agc tct	tct gcc tcc	cct	331
Ser Ser Gly	Asp Leu Ser	Pro Ser Pro	Pro Ser Ser	Ala Ser Pro		
	25		30		35	
gcc tgg acc	tct gag gag	gag gga ctg	ggg gat cag	cca ccc cag	cct	379
Ala Trp Thr	Ser Glu Glu	Glu Gly Leu	Gly Asp Gln	Pro Pro Gln	Pro	
	40		45		50	
gat cag gac	tcc agt ggc	atc cag agt	tta acg ccc	cca tcc atc	ctg	427
Asp Gln Asp	Ser Ser Gly	Ile Gln Ser	Leu Thr Pro	Pro Ser Ile	Leu	
	55		60		65	70
aag cgg gct	cct cgg gag	cgt ccg ggt	cac gtg gcc	ttc gat ggc	atc	475
Lys Arg Ala	Pro Arg Glu	Arg Pro Gly	His Val Ala	Phe Asp Gly	Ile	
	75		80		85	
act gtc tac	tat ttc ccg	cgg tgc cag	gga ttc acc	agt gtg ccc	agc	523
Thr Val Tyr	Tyr Phe Pro	Arg Cys Gln	Gly Phe Thr	Ser Val Pro	Ser	
	90		95		100	
cat ggt ggc	tgt acc ctg	ggc atg gct	tct cgt cat	agc acc tgc	cgc	571
His Gly Gly	Cys Thr Leu	Gly Met Ala	Ser Arg His	Ser Thr Cys	Arg	
	105		110		115	
ctc ttc tcc	tta gcc gag	ttt aaa cag	gag cag ttc	cgg gct cgg	cgt	619
Leu Phe Ser	Leu Ala Glu	Phe Lys Gln	Glu Gln Phe	Arg Ala Arg	Arg	
	120		125		130	
gag aag ctc	cgt cgg cgt	tta aag gag	gag aag cta	gag atg ctg	aaa	667
Glu Lys Leu	Arg Arg Arg	Leu Lys Glu	Glu Lys Leu	Glu Met Leu	Lys	
	135		140		145	150
tgg aag ctt	tca gtg tcc	gga gtt ccg	gag gca ggg	gca gac gtg	ccg	715
Trp Lys Leu	Ser Val Ser	Gly Val Pro	Glu Ala Gly	Ala Asp Val	Pro	

155								160				165					
ctc	aca	gtg	gac	gcc	atc	gat	gac	gct	tct	gta	gag	gag	gac	ttg	gca	763	
Leu	Thr	Val	Asp	Ala	Ile	Asp	Asp	Ala	Ser	Val	Glu	Glu	Asp	Leu	Ala		
170				175				180									
gtg	gcc	gtg	gca	ggc	ggc	cgc	ctg	gag	gaa	gag	aat	ttc	cta	cag	ccc	811	
Val	Ala	Val	Ala	Gly	Gly	Arg	Leu	Glu	Glu	Ala	Asn	Phe	Leu	Gln	Pro		
185				190				195									
tat	cca	cct	cgg	cag	cga	cgg	gcc	cta	ctt	cgc	gct	tcc	ggc	gtt	cga	859	
Tyr	Pro	Pro	Arg	Gln	Arg	Arg	Ala	Leu	Leu	Arg	Ala	Ser	Gly	Val	Arg		
200				205				210									
agg	att	gac	cga	gag	gag	aag	cac	gag	ctg	cag	gag	cta	cgc	caa	tcc	907	
Arg	Ile	Asp	Arg	Glu	Glu	Lys	His	Glu	Leu	Gln	Ala	Leu	Arg	Gln	Ser		
215				220				225				230					
cgg	gag	gat	tgt	ggc	tgt	cac	tgt	gat	ggc	gtc	tgt	gac	cct	gag	acc	955	
Arg	Glu	Asp	Cys	Gly	Cys	His	Cys	Asp	Gly	Val	Cys	Asp	Pro	Glu	Thr		
235				240				245									
tgc	agt	tgc	atc	ctg	gag	ggc	att	aaa	tgc	cag	atg	gat	cac	acg	tcc	1003	
Cys	Ser	Cys	Ile	Leu	Ala	Gly	Ile	Lys	Cys	Gln	Met	Asp	His	Thr	Ser		
250				255				260									
ttc	ccc	tgt	ggc	tgc	tgc	agc	gag	ggc	tgt	gag	aac	ccc	cat	ggc	cga	1051	
Phe	Pro	Cys	Gly	Cys	Cys	Ser	Glu	Gly	Cys	Glu	Asn	Pro	His	Gly	Arg		
265				270				275									
gtg	gaa	ttc	aat	cag	gag	aga	gtt	cag	aca	cac	ttc	atc	cac	acg	ctc	1099	
Val	Glu	Phe	Asn	Gln	Ala	Arg	Val	Gln	Thr	His	Phe	Ile	His	Thr	Leu		
280				285				290									
acc	cgc	ctg	cag	atg	gag	cag	ggc	gag	agg	gag	agt	ttg	ggg	gac	ccg	gag	1147
Thr	Arg	Leu	Gln	Met	Glu	Gln	Gly	Ala	Glu	Ser	Leu	Gly	Asp	Pro	Glu		
295				300				305				310					
tcc	ccc	atg	gag	gac	gtt	cct	gtc	gaa	caa	acc	gtg	gtt	tcc	ccc	ttt	1195	
Ser	Pro	Met	Glu	Asp	Val	Pro	Val	Glu	Gln	Thr	Val	Val	Ser	Pro	Phe		
315				320				325									
cct	cct	tcc	aaa	ccc	act	atg	agc	aat	gac	ctg	ggg	gac	agc	agc	tgt	1243	
Pro	Pro	Ser	Lys	Pro	Thr	Met	Ser	Asn	Asp	Leu	Gly	Asp	Ser	Ser	Cys		
330				335				340									
ggc	agc	gac	atg	aca	gac	tct	tcc	acg	acc	tac	tcc	tct	ggc	ggc	agt	1291	
Gly	Ser	Asp	Met	Thr	Asp	Ser	Ser	Thr	Thr	Tyr	Ser	Ser	Gly	Gly	Ser		
345				350				355									
ggc	agc	cgc	agc	gag	gct	ccg	aac	cat	ctt	gcc	cac	ccc	agc	ctg	cca	1339	
Gly	Ser	Arg	Ser	Glu	Ala	Pro	Asn	His	Leu	Ala	His	Pro	Ser	Leu	Pro		
360				365				370									
ggc	tcc	agc	ttc	cgg	tct	ggc	ata	gat	gaa	gac	agc	ctg	gaa	cag	atc	1387	
Gly	Ser	Ser	Phe	Arg	Ser	Gly	Ile	Asp	Glu	Asp	Ser	Leu	Glu	Gln	Ile		
375				380				385				390					
ctg	aat	ttc	agt	gac	tct	gac	ctc	ggc	att	gag	gaa	gaa	gag	gag	gag	1435	
Leu	Asn	Phe	Ser	Asp	Ser	Asp	Leu	Gly	Ile	Glu	Glu	Glu	Glu	Glu	Glu		

395	400	405	
gga ggg agt gtg ggc aac ttg gat aac ctc agc tgt ttt cat ttg gct Gly Gly Ser Val Gly Asn Leu Asp Asn Leu Ser Cys Phe His Leu Ala 410 415 420			1483
gac atc ttt ggt acc ggt gac ccc ggc agc ctg gct agc tgg aca cac Asp Ile Phe Gly Thr Gly Asp Pro Gly Ser Leu Ala Ser Trp Thr His 425 430 435			1531
agc cag ttt ggc tct agc ctt cca tcg ggc atc cta gat gag aat gcc Ser Gln Phe Gly Ser Ser Leu Pro Ser Gly Ile Leu Asp Glu Asn Ala 440 445 450			1579
aac ctg gac gcc agc tgc ttc cta agc agc gga ctc gaa ggg ttg aga Asn Leu Asp Ala Ser Cys Phe Leu Ser Ser Gly Leu Glu Gly Leu Arg 455 460 465 470			1627
gaa ggt agc ctc ccc agc agt tct ggg tcc cct gag ggg gaa gcc gcc Glu Gly Ser Leu Pro Ser Ser Ser Gly Ser Pro Glu Gly Glu Ala Ala 475 480 485			1675
cag agc agc tcc ttg gac ctc agt tta tcc tcc tgt gac tcc ttt gag Gln Ser Ser Ser Leu Asp Leu Ser Leu Ser Ser Cys Asp Ser Phe Glu 490 495 500			1723
ctt ctc caa tct ctg cca gat tat agt ctg ggg cct cac tat act tcc Leu Leu Gln Ser Leu Pro Asp Tyr Ser Leu Gly Pro His Tyr Thr Ser 505 510 515			1771
cga agg gta tct ggc agc ctg gac agc ctt gag acc ttc cac cct tcg Arg Arg Val Ser Gly Ser Leu Asp Ser Leu Glu Thr Phe His Pro Ser 520 525 530			1819
ccc agc ttc tct cca ccg agg gat gcc agc ttc ctg gat tct ctc ata Pro Ser Phe Ser Pro Pro Arg Asp Ala Ser Phe Leu Asp Ser Leu Ile 535 540 545 550			1867
ggc ctg tct gag ccg gtt aca gat gtc ctg gcg ccc ctt ctg gag agc Gly Leu Ser Glu Pro Val Thr Asp Val Leu Ala Pro Leu Leu Glu Ser 555 560 565			1915
cag ttt gag gac act gct gtg gtg cct ttg gac cct gtg cct gtg Gln Phe Glu Asp Thr Ala Val Val Pro Leu Asp Pro Val Pro Val 570 575 580			1960
taaggattga gatgactttt tcctgccctg agaccctggt gctgcttttt atgtgatctt			2020
ggtgtccccc aaggtctgtg tatgtaacgg tctcccgtgg gctgggtctg ccccggtgcc			2080
atgtgggcaa tccctctattt ttacagtaac actctagatt tattttatttt tttatgtttt			2140
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aacagaggtc tcccacctcc tactgtatgc ctggaggagg aaggggcggg gttcacatcc			2260
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Ile Thr Ala Lys Lys Gly Gly Thr Ser Lys Pro Arg Ala Ser Gly Thr	
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ccc cca ccg tcc tcc tcc gtt gcc atc agc aac cac gtc acc cca cca	679
Pro Pro Pro Ser Ser Ser Val Ala Ile Ser Asn His Val Thr Pro Pro	
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Pro Ile Pro Lys Ser Asn His Gly Ser Asn Asp Ser Asp Ile Leu Leu	
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Asp Leu Asp Ser Pro Ala Pro Val Pro Thr Ser Ala Pro Ala Pro Ala	
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 acc aaa gtc agc cag gcc gtg ctg aag gcc aag att cag aaa ctg tct	630
Thr Lys Val Ser Gln Ala Val Leu Lys Ala Lys Ile Gln Lys Leu Ser	
190 195 200	
 gag agc ctg gag tcc tgc act ggt gcc ctg gat gaa ctt agt gag cag	678
Glu Ser Leu Glu Ser Cys Thr Gly Ala Leu Asp Glu Leu Ser Glu Gln	

205

210

215

ctg gaa tcc cgg gtc cag ctc tgt acc aag gcc ggc cgt ggt cac aac 726
 Leu Glu Ser Arg Val Gln Leu Cys Thr Lys Ala Gly Arg Gly His Asn
 220 225 230

ctc agg aac tcc cct gat ctg gat gca gcg ttg ttt ttc taa 768
 Leu Arg Asn Ser Pro Asp Leu Asp Ala Ala Leu Phe Phe *
 235 240 245

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<211> 246

<212> PRT

<213> Eukaryote

<400> 32

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 20 25 30
 Val Leu Arg Leu Arg Glu Val Ala Arg Arg Leu Glu Arg Leu Arg Arg
 35 40 45
 Arg Ser Leu Ala Ala Asn Val Ala Gly Ser Ser Leu Ser Ala Ala Gly

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Ala Leu Ala Ala Ile Val Gly Leu Ser Leu Ser Pro Val Thr Leu Gly		
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Ala Ser Leu Val Ala Ser Ala Val Gly Leu Gly Val Ala Thr Ala Gly		
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Gly Ala Val Thr Ile Thr Ser Asp Leu Ser Leu Ile Phe Cys Asn Ser		
100	105	110
Arg Glu Val Arg Arg Val Gln Glu Ile Ala Ala Thr Cys Gln Asp Gln		
115	120	125
Met Arg Glu Leu Leu Ser Cys Leu Glu Phe Phe Cys Gln Trp Gln Gly		
130	135	140
Arg Gly Asp Arg Gln Leu Leu Gln Ser Gly Arg Asp Ala Ser Met Ala		
145	150	155
Leu Tyr Asn Ser Val Tyr Phe Ile Val Phe Phe Gly Ser Arg Gly Phe		
165	170	175
Leu Ile Pro Arg Arg Ala Glu Gly Ala Thr Lys Val Ser Gln Ala Val		
180	185	190
Leu Lys Ala Lys Ile Gln Lys Leu Ser Glu Ser Leu Glu Ser Cys Thr		
195	200	205
Gly Ala Leu Asp Glu Leu Ser Glu Gln Leu Glu Ser Arg Val Gln Leu		
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Cys Thr Lys Ala Gly Arg Gly His Asn Leu Arg Asn Ser Pro Asp Leu		
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<400> 33

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 <212> DNA
 <213> Eukaryote

<220>
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 <223> r = G or A
 y = C or T
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 w = A or T
 n = A, T, G, or C

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 <211> 796
 <212> DNA
 <213> Eukaryote

<220>
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 <222> (1)...(796)

<223> n = A, T, G, or C

<400> 35

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<210> 36

<211> 214

<212> PRT

<213> Eukaryote

<400> 36

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			20					25					30		
Tyr	Lys	Tyr	Glu	Gly	Trp	Cys	Gly	Arg	Gln	Cys	Arg	Arg	Lys	Gly	Gln
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Ser	Gln	Arg	Lys	Gly	Ser	Ala	Asp	Trp	Arg	Glu	Arg	Arg	Glu	Gln	Ala
	50					55				60					
Asp	Thr	Val	Asp	Leu	Asn	Trp	Cys	Val	Ile	Ser	Asp	Met	Glu	Val	Ile
65					70					75				80	
Glu	Leu	Asn	Lys	Cys	Thr	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys
			85					90					95		
Pro	Pro	Ser	Phe	Asp	Gly	Val	Pro	Glu	Phe	Asn	Ala	Ser	Leu	Pro	Arg
		100						105					110		
Arg	Arg	Asp	Pro	Ser	Leu	Glu	Glu	Ile	Gln	Lys	Lys	Leu	Glu	Ala	Ala
		115					120					125			
Glu	Glu	Arg	Arg	Lys	Tyr	Gln	Glu	Ala	Glu	Leu	Leu	Lys	His	Leu	Ala
	130					135				140					
Glu	Lys	Arg	Glu	His	Glu	Arg	Glu	Val	Ile	Gln	Lys	Ala	Ile	Glu	Glu
145				150					155					160	
Asn	Asn	Asn	Phe	Ile	Lys	Met	Ala	Lys	Glu	Lys	Leu	Ala	Gln	Lys	Met
			165					170					175		
Glu	Ser	Asn	Lys	Glu	Asn	Arg	Glu	Ala	His	Leu	Ala	Ala	Met	Leu	Glu
		180					185					190			
Arg	Leu	Gln	Glu	Lys	Asp	Lys	His	Ala	Glu	Glu	Val	Arg	Lys	Asn	Lys
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<210> 37

<211> 3976

<212> DNA

<213> Eukaryote

<220>

<221> CDS

<400> 37

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Ala	Asp	Gly	Ala	Ser	Ser	Val	
		5				10	
cac	gac	aac	ccc	gcg	ctg	tta	152
His	Asp	Asn	Pro	Ala	Leu	Leu	
	20				25		
cgc	tgc	gtc	tac	atc	ctc	gac	200
Arg	Cys	Val	Tyr	Ile	Leu	Asp	
35				40			
ggc	atc	aac	cga	tgg	agg	ttc	248
Gly	Ile	Asn	Arg	Trp	Arg	Phe	
			55			60	
aca	agc	tta	aga	aag	ctg	aat	296
Thr	Ser	Leu	Arg	Lys	Leu	Asn	
			70			75	
cca	gct	gat	gtg	ttc	cca	agg	344
Pro	Ala	Asp	Val	Phe	Pro	Arg	
		85				90	
ttg	acc	ttt	gaa	tat	gac	tcc	392
Leu	Thr	Phe	Glu	Tyr	Asp	Ser	
100					105		
gcc	att	atg	aag	atg	gcc	aag	440
Ala	Ile	Met	Lys	Met	Ala	Lys	
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Asn	Ser	His	Thr	Leu	Tyr	Asp	
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cag	aaa	cca	ccc	ctt	acc	tac	536
Gln	Lys	Pro	Pro	Leu	Thr	Tyr	
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atg	gag	ctg	ccc	aag	aag	cca	584
Met	Glu	Leu	Pro	Lys	Lys	Pro	
		165				170	
gag	aac	tgc	aga	gct	gag	atc	632
Glu	Asn	Cys	Arg	Ala	Glu	Ile	
	180				185		
gtg	cct	tcc	tta	gag	gaa	ctg	680
Val	Pro	Ser	Leu	Glu	Glu	Leu	
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gct	gtt	tgg	caa	gga	gga	gag	728

Ala	Val	Trp	Gln	Gly	Gly	Glu	Thr	Glu	Ala	Leu	Ala	Arg	Leu	Asp	Lys	
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cac	ttg	gaa	cgg	aag	gcc	tgg	gtt	gcc	aac	tat	gag	aga	cct	cgg	atg	776
His	Leu	Glu	Arg	Lys	Ala	Trp	Val	Ala	Asn	Tyr	Glu	Arg	Pro	Arg	Met	
			230					235					240			
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Asn	Ala	Asn	Ser	Leu	Leu	Ala	Ser	Pro	Thr	Gly	Leu	Ser	Pro	Tyr	Leu	
		245					250					255				
cgc	ttt	ggc	tgc	ctc	tcc	tgc	cgc	ctc	ttc	tac	tac	cgc	ctg	tgg	gac	872
Arg	Phe	Gly	Cys	Leu	Ser	Cys	Arg	Leu	Phe	Tyr	Tyr	Arg	Leu	Trp	Asp	
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Leu	Tyr	Arg	Lys	Val	Lys	Arg	Asn	Ser	Thr	Pro	Pro	Leu	Ser	Leu	Phe	
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Gly	Gln	Leu	Leu	Trp	Arg	Glu	Phe	Phe	Tyr	Thr	Ala	Ala	Thr	Asn	Asn	
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ccc	agg	ttt	gac	cga	atg	gag	ggg	aac	ccc	atc	tgc	atc	cag	atc	ccc	1016
Pro	Arg	Phe	Asp	Arg	Met	Glu	Gly	Asn	Pro	Ile	Cys	Ile	Gln	Ile	Pro	
			310					315					320			
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Trp	Asp	Arg	Asn	Pro	Glu	Ala	Leu	Ala	Lys	Trp	Ala	Glu	Gly	Lys	Thr	
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Gly	Phe	Pro	Trp	Ile	Asp	Ala	Ile	Met	Thr	Gln	Leu	Arg	Gln	Glu	Gly	
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Trp	Ile	His	His	Leu	Ala	Arg	His	Ala	Val	Ala	Cys	Phe	Leu	Thr	Arg	
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Gly	Asp	Leu	Trp	Val	Ser	Trp	Glu	Ser	Gly	Val	Arg	Val	Phe	Asp	Glu	
				375					380					385		
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Leu	Leu	Leu	Asp	Ala	Asp	Phe	Ser	Val	Asn	Ala	Gly	Ser	Trp	Met	Trp	
			390					395					400			
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		405					410					415				
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Trp	Asn	Ala	Pro	Glu	Ser	Val	Gln	Lys	Ala	Ala	Lys	Cys	Ile	Ile	Gly		
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Val	Asp	Tyr	Pro	Arg	Pro	Ile	Val	Asn	His	Ala	Glu	Thr	Ser	Arg	Leu		
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aac	att	gag	cgg	atg	aag	cag	atc	tac	caa	cag	ctg	tca	cga	tac	cgg	1544	
Asn	Ile	Glu	Arg	Met	Lys	Gln	Ile	Tyr	Gln	Gln	Leu	Ser	Arg	Tyr	Arg		
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aca	ggc	ccc	aga	cca	ctg	tcc	agt	ggc	cca	gcc	tcc	ccc	aaa	cgc	aag	1688	
Thr	Gly	Pro	Arg	Pro	Leu	Ser	Ser	Gly	Pro	Ala	Ser	Pro	Lys	Arg	Lys		
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Leu	Glu	Ala	Ala	Glu	Glu	Pro	Pro	Gly	Glu	Glu	Leu	Ser	Lys	Arg	Ala		
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aga	gtg	aca	gtg	act	cag	atg	cct	gcc	cag	gag	cca	cca	agc	aag	gac	1784	
Arg	Val	Thr	Val	Thr	Gln	Met	Pro	Ala	Gln	Glu	Pro	Pro	Ser	Lys	Asp		
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Ser	*																
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<211> 579

<212> PRT

<213> Eukaryote

<400> 38

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			20					25					30		
Cys	Val	Arg	Cys	Val	Tyr	Ile	Leu	Asp	Pro	Trp	Phe	Ala	Ala	Ser	Ser
		35					40					45			
Ser	Val	Gly	Ile	Asn	Arg	Trp	Arg	Phe	Leu	Leu	Gln	Ser	Leu	Glu	Asp
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Leu	Asp	Thr	Ser	Leu	Arg	Lys	Leu	Asn	Ser	Arg	Leu	Phe	Val	Val	Arg
65					70					75					80
Gly	Gln	Pro	Ala	Asp	Val	Phe	Pro	Arg	Leu	Phe	Lys	Glu	Trp	Gly	Val
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Thr	Arg	Leu	Thr	Phe	Glu	Tyr	Asp	Ser	Glu	Pro	Phe	Gly	Lys	Glu	Arg
			100					105					110		
Asp	Ala	Ala	Ile	Met	Lys	Met	Ala	Lys	Glu	Ala	Gly	Val	Glu	Val	Val
		115					120					125			
Thr	Glu	Asn	Ser	His	Thr	Leu	Tyr	Asp	Leu	Asp	Arg	Ile	Ile	Glu	Leu
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Asn	Gly	Gln	Lys	Pro	Pro	Leu	Thr	Tyr	Lys	Arg	Phe	Gln	Ala	Leu	Ile
145					150					155					160
Ser	Arg	Met	Glu	Leu	Pro	Lys	Lys	Pro	Val	Gly	Ala	Val	Ser	Ser	Gln
			165						170					175	
His	Met	Glu	Asn	Cys	Arg	Ala	Glu	Ile	Gln	Glu	Asn	His	Asp	Asp	Thr
			180					185					190		
Tyr	Gly	Val	Pro	Ser	Leu	Glu	Glu	Leu	Gly	Phe	Pro	Thr	Glu	Gly	Leu
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Gly	Pro	Ala	Val	Trp	Gln	Gly	Gly	Glu	Thr	Glu	Ala	Leu	Ala	Arg	Leu
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Asp	Lys	His	Leu	Glu	Arg	Lys	Ala	Trp	Val	Ala	Asn	Tyr	Glu	Arg	Pro
225					230					235					240
Arg	Met	Asn	Ala	Asn	Ser	Leu	Leu	Ala	Ser	Pro	Thr	Gly	Leu	Ser	Pro
			245						250					255	
Tyr	Leu	Arg	Phe	Gly	Cys	Leu	Ser	Cys	Arg	Leu	Phe	Tyr	Tyr	Arg	Leu
			260					265					270		
Trp	Asp	Leu	Tyr	Arg	Lys	Val	Lys	Arg	Asn	Ser	Thr	Pro	Pro	Leu	Ser
		275					280					285			
Leu	Phe	Gly	Gln	Leu	Leu	Trp	Arg	Glu	Phe	Phe	Tyr	Thr	Ala	Ala	Thr
	290					295					300				
Asn	Asn	Pro	Arg	Phe	Asp	Arg	Met	Glu	Gly	Asn	Pro	Ile	Cys	Ile	Gln
305					310					315					320
Ile	Pro	Trp	Asp	Arg	Asn	Pro	Glu	Ala	Leu	Ala	Lys	Trp	Ala	Glu	Gly
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Lys Thr Gly Phe Pro Trp Ile Asp Ala Ile Met Thr Gln Leu Arg Gln
 340 345 350
 Glu Gly Trp Ile His His Leu Ala Arg His Ala Val Ala Cys Phe Leu
 355 360 365
 Thr Arg Gly Asp Leu Trp Val Ser Trp Glu Ser Gly Val Arg Val Phe
 370 375 380
 Asp Glu Leu Leu Leu Asp Ala Asp Phe Ser Val Asn Ala Gly Ser Trp
 385 390 395 400
 Met Trp Leu Ser Cys Ser Ala Phe Phe Gln Gln Phe Phe His Cys Tyr
 405 410 415
 Cys Pro Val Gly Phe Gly Arg Arg Thr Asp Pro Ser Gly Asp Tyr Ile
 420 425 430
 Arg Arg Tyr Leu Pro Lys Leu Lys Gly Phe Pro Ser Arg Tyr Ile Tyr
 435 440 445
 Glu Pro Trp Asn Ala Pro Glu Ser Val Gln Lys Ala Ala Lys Cys Ile
 450 455 460
 Ile Gly Val Asp Tyr Pro Arg Pro Ile Val Asn His Ala Glu Thr Ser
 465 470 475 480
 Arg Leu Asn Ile Glu Arg Met Lys Gln Ile Tyr Gln Gln Leu Ser Arg
 485 490 495
 Tyr Arg Gly Leu Cys Leu Leu Ala Ser Val Pro Ser Cys Val Glu Asp
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 Leu Ser His Pro Val Ala Glu Pro Gly Ser Ser Gln Ala Gly Ser Ile
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 Ser Asn Thr Gly Pro Arg Pro Leu Ser Ser Gly Pro Ala Ser Pro Lys
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 Lys Asp Ser

<210> 39
 <211> 629
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(629)
 <223> r = G or A
 y = C or T
 n = A,T,C or G

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<210> 40
 <211> 2461

<212> DNA
<213> Eukaryote

<400> 40

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aattatgggg agcaaccaac ttttctgttc tgtttttgaa gtgctactat gaaccattca 660
gagtcgtatt tttttttttt aaaattttgg ccagatatcc ccagctaattg aaaaatagtc 720
accattcctt gaaaaagttg gaagctagaa cccccaattc caaattattg ttgaagatgt 780
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<210> 41
<211> 1131
<212> DNA
<213> Eukaryote

<220>
<221> misc_feature
<222> (1)...(1131)
<223> r = G or A
n = A,T,C or G

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cattttctaa	cagaggggaa	cacagacaga	cagacagaca	gacagacaca	caaacacaca	180
aacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	240
cacaccccag	actgcgtagt	tggcataaca	tacagcttgc	atgggaagca	gccccctgcr	300
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ttcatccgcg	tgagtgtttg	tatccatgat	gattccagca	tgaagtacgt	agcacactcc	720
agttaggaga	aattttttaa	agatacaaga	ctagcgtggt	ggtgagatga	gatagtcttc	780
tcgtgtctcg	agcaacctga	aggggcaata	aggacaaaaga	aggccatgtg	gcagggttag	840
ccccctccag	accaggggta	caacggacag	ttgtgggtgag	cctcggaag	gcaggggtaa	900
ccttccctct	ccgttcttca	cccatggcca	gagcaaggca	ggtagtgaag	gggatatgct	960
tgatgcagaa	aagccagctc	aggcatggca	ggtgggattt	atagctgggt	ttgttttaaag	1020
cgaaggcctg	atatttgata	aatgcagtaa	ccagcgggtg	agagtgacaa	gcccttaaata	1080
gcgaacatta	atcaaaggag	aacttaaacg	gcccccttta	cagaaggact	t	1131

<210> 42

<211> 1473

<212> DNA

<213> Eukaryote

<400> 42

cgagtttttt	ttttttatgt	actttgaaaa	tatatattaa	aacattaaaa	attctatatatt	60
taaaacatat	attatatgtt	aattggtaca	cttaaataga	acctgtattt	acaataggct	120
tctgatgtgg	ttaagtttta	atgccaat	ttttttcaat	aacataatta	tataaatata	180
ctaaaatata	ataaatat	ttcttgtttt	acatgggtgaa	taatatcttt	accatagaga	240
gaacaaggcc	acagacattt	acttacagtt	tcaatgggaa	tcactataaa	aagcatcagg	300
cctgctgcca	tgcatgaaac	acttctgcca	aaaagagacc	acagcaagac	tttcagaaca	360
gaacagaaaca	gaacaggagc	gaaacagaac	gaacagaaac	agaggagaga	ttttaacaaa	420
tcaatctcag	gtcaacataa	accaccgaca	tggagctatg	atgtatctta	gtgggtatga	480
gagccagcca	ctgaccacac	agttgcggag	ggtctcctat	gaagccacct	aatcgacctg	540
gcccttcgaa	taccgtgaga	ttgtgatggg	gctcctttta	tttgtttgac	taacgtctct	600
cagaatgaag	ctgcaaaaaa	ttagcatata	gcagatattc	aaagcattcc	ttaatagggt	660
aaaaatgatg	acagagatta	atgttgtcaa	acggcacaaa	acaatctagg	ctacgtgaag	720
tcttccaaaa	acaggggatt	cagtgggact	ccagaagaca	gactagtctt	aaaggaacag	780
ttgaacaaaa	agaaactatt	tgctgatggg	atcttcactc	cctgagtcac	agtggacagc	840
cactttgttt	caccttttcc	actcctaaga	tgaagcaatt	gtttgcctct	ttttctgatg	900
cccaggagcc	cagtcaggta	accactaaca	cattcgcgct	ggcggaaaac	ctcactaggg	960
aatgggctt	aacactagtt	ctcattgggg	ccattcattc	aggcttccag	cttgacttct	1020
cctaacccca	agaggtaaag	tgtagaaggg	acccttgtgc	tgaatggaca	gaactatcag	1080
gagctttctg	tgctcttcac	ttaagcagta	tttctctctg	tggtcttctg	tctttcacag	1140
tgaaagcacc	ttcctatgcc	ttgtcattct	agcccttaca	gacagacatt	gctcattctg	1200
cctaagtttt	ggtgcttttt	ctggttttgt	ttgtttgttt	tcttctttct	tttttctttt	1260
cacccaaatg	tctcaaaaaa	ataaataaat	aaaacctagg	cttctgaag	tctaagcgca	1320
aagaaagtta	agtctcttca	cagcaaacat	ttcccatcat	gctgcactga	tagcatcact	1380
gctatgccat	atgtggatcc	aaagctgctc	cagggttaatc	caactttatc	cataattatt	1440
taaaatggga	tggaggccat	aaatggattt	gag			1473

<210> 43

<211> 326

<212> DNA

<213> Eukaryote

<400> 43

agtctgggac	taaaacgtca	cagcagaaaa	aaaataaaaa	aaaataattt	gcttttttctt	60
tcttttcattt	agcagcataa	ataagtgttg	ccactgggag	tacagtacag	gggtgggaca	120
acgatcccgt	atgtgaagac	ctacttctag	caccagcatc	aagaactaaa	tccacctcag	180

gactcacaga	accaggaca	acttgccatc	tttgagcaac	atatgcattg	aagagtgtat	240
atagaagcaa	cagtaaatag	attaacagag	gctaatactg	tgattgattg	acattggcaa	300
tggttgggcaa	aaaaaaaaaa	aaaaaa				326

<210> 44
 <211> 429
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1) ... (429)
 <223> n = A,T,C or G

<400> 44						
acttgataaa	attgtatttt	tttttctaca	gtcatttgta	caatttggtta	caaaaccata	60
gaagactaca	acttgtttta	aatcattttt	ggctctgcaa	tatgtaaaat	ctgtgggtgca	120
attatcatgt	atttacaggg	ccttgtagt	catttttcaat	gattatttca	acaatgtcac	180
actctcaaca	taagacatgg	cttaagacaa	atatattagt	acatanatat	tctgagaaca	240
tattttccatn	aatggaaagt	ngctgcta	acanatag	aatatacata	agntgttttc	300
tagcttttta	aaacagtttt	taaaatggna	angtgaaaaa	agagccccta	ggancatttt	360
atcccaaaaa	aatccttacn	aaatattnaa	ggggccaggg	ggggaattaa	aaatctaaaa	420
anggtgggtc						429

<210> 45
 <211> 1210
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1) ... (1210)
 <223> r = G or A
 m = A or C
 s = G or C
 w = A or T

<400> 45						
aargggrrcca	ccccaccgsg	ctaaaggccc	agggggcccc	cccttgaggm	cccagggggt	60
ttggcccmcc	ccctcaccce	aatgggtctg	caatgaccce	gggtactcaca	acatgttcca	120
ggaggagmct	ggggccagga	ttttgaccag	aggggtatggg	aaggggaaagg	ggagaagaaa	180
tcgacatttta	tttttattat	ttatttttaa	tgtttacawt	ttctttgtgt	tggtccaagc	240
cctgaataga	aacagatagc	attaaaggac	tctgttccca	ccccttctct	gtctctctct	300
ccccacttg	tgctaactta	ggataaact	ctctatttcg	ttttgtttct	aaagtgtatt	360
gtggacttgt	gccgtgtgaa	ctgcattaaa	aagggttctgt	tttcaaagat	cgattgtcgt	420
tcctgtgggg	acagtggctc	ctaagaaatc	tgcatgttag	gagaagacaa	tgaaagaccc	480
tgccctgtc	tctcaaaaact	taactctctg	tatgatttaa	aaaaaaattc	catttacttt	540
actttgtggt	tacttgattt	tgaggaagaa	aatattcaac	tttgtataaa	gactaggtat	600
cagggtttct	tttgcaagtgg	gagttgtata	tatatcgtat	tttggtatat	cgtagaaaact	660
caagctttat	gcattccgtat	ttgggatatg	tcaatgacgt	gcagtgaat	ttgtctattag	720
accctggagg	caaacgagtt	gtacaagggt	ttatggctcc	atggggaatt	ctaatttctt	780
ttctggggac	cttttgtccc	gtttttacag	taatggtgaa	atgggtcctag	gaggggtctct	840
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ttgaggagta	tctctgctca	gaagcatctg	tggtgggtgtg	tggtgctgtg	ttctgtgtac	960
tgtgtgtgac	acaagcctac	agtatttgca	ctaaggaaaag	ctgttttagag	cttgctgcta	1020
tggagggaag	aacatattaa	aacttatttt	ccctcggggw	tttwtcwmgt	tttatgtwct	1080
tgtgtgtctg	ttggctttcc	tactttccac	tgagtagcat	tttgtagaat	aaaatgaatt	1140
aagatcagmw	rwrwrmaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa						1210

<210> 46
 <211> 700
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 46
 aattccccat ggagccataa aaccttgtac aactcgtttg cctccagggt ctaatagcaa 60
 atttcactgc acgtcattga catatcccaa atacggatgc ataaagcttg agtttctacg 120
 atataccaaa atacgatata tatacaactc ccactgcaaa agaaaccctg atacctagtc 180
 ttatatacaa gttgaatatt ttcttctca aaatcaagta accacaaagt aaagtaaagt 240
 gaattttttt taaatcatac agagagttaa gttttgagag acagggccag ggtctttcat 300
 tgtcttctcc tacaatgcag atttcttagg agccactgtc cccacaggaa cgacaatcga 360
 tctttgaaaa cagaaccttt ttaatgcagt tcacacggca caagtccaca aatcactttn 420
 gaaacaaaac gaaatagaga gtgttatcct aagtnagcac aagtgggggn gagngagaca 480
 gagaaggggt gggaacagag tcctttaatg cnatctgttt ctattcaggc ttggaacaac 540
 acaaagaaat gtaaacattt agnataaata atagaataaa tgtcgggttc ttctcccctg 600
 tcccttccca taccnctgg caaaatctgn cccaggctct cccggaacat ggtgngagta 660
 cctgggtcca ttgnagncca tttggngagg gcgtggccaa 700

<210> 47
 <211> 3316
 <212> DNA
 <213> Eukaryote

<220>
 <221> CDS
 <222> (94)...(993)

<400> 47
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 tttcccgtga gcccgagccc ggcaaatggg cga atg aag aag gag agc agg gac 114
 Met Lys Lys Glu Ser Arg Asp
 1 5
 atg gac tgc tat ctg cgt cgc ctc aaa cag gag ctg atg tcc atg aag 162
 Met Asp Cys Tyr Leu Arg Arg Leu Lys Gln Glu Leu Met Ser Met Lys
 10 15 20
 gag gtg ggg gat ggc tta cag gat cag atg aac tgc atg atg ggt gca 210
 Glu Val Gly Asp Gly Leu Gln Asp Gln Met Asn Cys Met Met Gly Ala
 25 30 35
 ctt caa gaa ctg aag ctc tta cag gtg cag aca gca ttg gaa cag ctg 258
 Leu Gln Glu Leu Lys Leu Leu Gln Val Gln Thr Ala Leu Glu Gln Leu
 40 45 50 55
 gag atc tct gga ggc gcg ccc acc ttc agc tgc cct aag agc tca cag 306
 Glu Ile Ser Gly Gly Ala Pro Thr Phe Ser Cys Pro Lys Ser Ser Gln
 60 65 70
 gaa cag acc gag tgc cct cgc tgg cag ggt agt gga ggg cct gct ggg 354
 Glu Gln Thr Glu Cys Pro Arg Trp Gln Gly Ser Gly Gly Pro Ala Gly
 75 80 85
 ctt gct gcc tgt ccc tcc tcc agt caa cca tct ttt gac ggc agc ccc 402

[illegible]

ctatgatatt cctccattac cttacccaag acctcatttg aacatttctat atgcaaagg 1393
 gcatttagcc ctcagggttc ccagaggaac tcccaataaa gacctgtctc agggaccccc 1453
 aaccattttt taatgggtctg cttccctgac aaggcactga tgcaggcaag gggtttgttt 1513
 ttgttttaag ggttgggtatc ccagaatgga gcaccggaaa taggaaaatc cctattttata 1573
 gcccttcccta ggaccaagat ttcacccatg gctgggtgct ggggacgcag aacaagcaga 1633
 ggggtgtgcg tgcgtgcgtg cgtgcgtgcg tgcattgtgtt gttgaggaag cctgagatgc 1693
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 cagccatctc tgagagcaca ctcggctgcc aggaggaaaa acagggtcagg ccaatctcat 1813
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 ataataccca tacattgaga acatttctta gtctacatct catagtcatc cagcgaactg 1993
 gacacatcta cccgcatcac cctggaggtc aacaggggac cctgaggggtg gggctgatgc 2053
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 cccacccctt agccaggaga gaacaaagta ggccctgtt caagcccagc tcggagggtg 2173
 ccttagctcc tccttcgccc cctcctgcag acccagctca gcttgatgag gtgtgacaac 2233
 tgcaattaga ggcaagccgc ctgctgcccc cagagcatta agagcaaatt agagaagaaa 2293
 aatcacaaga gaagctcttc tgctgagct ctgactccc aggggactgg gtggaggaag 2353
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 gttcccacgc agttaaatga taggtggcct tttttttttt tttttaatct gtagcttttt 2473
 gtcaggcaat gtgcctatct ctttcagaac aattaatcag tgggggtcaaa gggccctgcc 2533
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 cacagggtgc tgtcaccttg atctttattt ttctgttaca cccaggaaat ggttgctcat 3133
 tttaccagtg agactcggag aagttaatgc tttcaaggtc acacagtaca aagctgggat 3193
 tgaacagtt tgtaactgac ttccaatctt gtgttcatgc tacctggcaa actgtccata 3253
 tttgctccac agccagatcc agaataacat ttgtctctc tcgtgcaaaa aaaaaaaaaa 3313
 aaa 3316

<210> 48

<211> 299

<212> PRT

<213> Eukaryote

<400> 48

Met Lys Lys Glu Ser Arg Asp Met Asp Cys Tyr Leu Arg Arg Leu Lys
 1 5 10 15
 Gln Glu Leu Met Ser Met Lys Glu Val Gly Asp Gly Leu Gln Asp Gln
 20 25 30
 Met Asn Cys Met Met Gly Ala Leu Gln Glu Leu Lys Leu Leu Gln Val
 35 40 45
 Gln Thr Ala Leu Glu Gln Leu Glu Ile Ser Gly Gly Ala Pro Thr Phe
 50 55 60
 Ser Cys Pro Lys Ser Ser Gln Glu Gln Thr Glu Cys Pro Arg Trp Gln
 65 70 75 80
 Gly Ser Gly Gly Pro Ala Gly Leu Ala Ala Cys Pro Ser Ser Ser Gln
 85 90 95
 Pro Ser Phe Asp Gly Ser Pro Lys Phe Pro Cys Arg Arg Ser Ile Cys
 100 105 110
 Gly Lys Glu Leu Ala Val Leu Pro Lys Thr Gln Met Pro Glu Asp Gln
 115 120 125
 Ser Cys Thr Gln Gln Gly Ile Glu Trp Val Glu Pro Asp Asp Trp Thr
 130 135 140
 Ser Thr Leu Met Ser Arg Gly Arg Asn Arg Gln Pro Leu Val Leu Gly

145 150 155 160
 Asp Asn Val Phe Ala Asp Leu Val Gly Asn Trp Leu Asp Leu Pro Glu
 165 170 175
 Leu Glu Lys Gly Gly Glu Arg Gly Glu Thr Gly Gly Ser Gly Glu Pro
 180 185 190
 Lys Gly Glu Lys Gly Gln Ser Arg Glu Leu Gly Arg Lys Phe Ala Leu
 195 200 205
 Thr Ala Asn Ile Phe Arg Lys Phe Leu Arg Ser Val Arg Pro Asp Arg
 210 215 220
 Asp Arg Leu Leu Lys Glu Lys Pro Gly Trp Met Thr Pro Met Val Ser
 225 230 235 240
 Glu Ser Arg Ala Gly Arg Ser Lys Lys Val Lys Lys Arg Ser Leu Ser
 245 250 255
 Lys Gly Ser Gly Arg Phe Pro Phe Ser Ser Thr Gly Glu Pro Arg His
 260 265 270
 Ile Glu Thr Pro Ala Thr Ser Ser Pro Lys Ala Leu Glu Pro Ser Cys
 275 280 285
 Arg Gly Phe Asp Ile Asn Thr Ala Val Trp Val
 290 295

<210> 49
 <211> 949
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(949)
 <223> r = A or G
 y = T or C
 m = A or C
 k = G or T
 s = G or C
 w = A or T
 b = G, C, or T; not A
 d = A, G, or T; not C
 h = A, C, or T; not G
 v = A, G, or C; not T
 n = A, T, G, or C

<400> 49
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 ttaccgatca ntgancaaag caagcacagc caaaatcgga cctcacctta attccgtctt 120
 cacacaaaaa taaaaaaacg gcaaaactcac ccccatTTTT aattttgttt ttaattttac 180
 ttacttattt tattttattta ttttttggca aaaaaatctc aggaatggcc ctgggccacc 240
 tactatatta atcatttttga taacatgaaa aatgatgggc tcttcctaat gaaaaascaa 300
 ggaaaggaaa aggccagggg aatgagctca aaattgatgc ccacktgagg agcatctggt 360
 gaataatcgc tcacktcctt cttccacagt accttgTTTT gatcatttcc acagcacatt 420
 tctcctccar aaacscgaaa aacacaascg tktgggttct gcatttttaa ggataarara 480
 raaaaagagg ttgggtatag taggacaggt tgtcagaaga gatgctgcta tggtcacgag 540
 gggccggttt cacctgctat tgttgctgcc tcttcagtt ccaactgcct tatgtccctt 600
 cctctctctt gtttttagctg ttacacatac agtaatacct gaatatccaa cggtatagtt 660
 cacaaggggg taatcaatgt taaatctaaa atagaattta aaaaaaaaag attttgacat 720
 aaaagagcct tgatttttaa aaaaaaagag agagatgtaa tttaaaaagt ttattataaa 780
 ttaaattcag caaaaatttg ctacaaagta tagagaagta taaaataaaa gttatyhggt 840
 tcaaamtavc dtrtcgamct cvtcvabccc grggaakccm ctaskkccbar hscggccccc 900
 accscssysk akmtycatk ttttgawwcc ctttagtgag ggttaanaa 949

<210> 50
 <211> 785

<212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(785)
 <223> n = A,T,C or G

<400> 50
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 cctctgcctt cccagtgcac aaagtctctg tcgctcccgg aacttggttg caatgcctat 120
 ttttcagctt tccccgcgt tctctaaact aactatttaa aggtctgcgg tcgcaaattgg 180
 tttgactaaa cgtaggatgg gacttaagtt gaacggcaga tatatttcac tgatcctcgc 240
 ggtgcaaata gcttacctgg tgcaggccgt gagagcagca ggcaagtgcg atgcagtctt 300
 taagggcttt tcagactggt tgctcaagct ggggtgacagc atggccaact acccgaggg 360
 cctggacgac aagacgaaca tcaagaccgt gtgcacatac tgggaggatt tccacagctg 420
 cacggtcaca gctcttacgg attgccagga aggggagaaa gatatgtggg ataaactgag 480
 aaaagaatcg aaaaacctca atatccaagg cagcttattc gaactctgcg gcagcggcaa 540
 cggggcgggc ggggtccctgc tcccggcgct ttccgtgctc ctggtgtctc tctcggcagc 600
 ttttagcgacc tggcttttct tctgagcacg gggccgggtc cccctccgc tcaccaccc 660
 acactcactc catgctcccg gaaaatcgag aggaaagagc cattcggtct ctaaggacgt 720
 tggttgattct ctggtgatat tgaaaacact catatgggga ttggtgggna aatcctgttt 780
 ctctc 785

<210> 51
 <211> 782
 <212> DNA
 <213> Eukaryote

<220>
 <221> misc_feature
 <222> (1)...(782)
 <223> y = C or T
 m = A or C
 k = G or T
 w = A or T
 n = A,T,C or G

<400> 51
 aaaccnagaa cccccctttg nagaaccntt gtttcttttc aagcccaagg aaggcggggc 60
 ccaacctttg gtgtnttttg aacaggcctt gaacaggagg ntwaggagaa atttccgggtt 120
 gtggaacccc aacaggaacc ccttggcacc cctggcccca aggttggtgma actttgggtt 180
 gcttaatttg gaccgttttt gccttgagga ttcatactt tttttgkgc ccttgtagc 240
 caagatgttg ggttttccca tcaacawtaa taacccttg ctttttgggg tgattccct 300
 ggggagtttc ctgatgaatt ccccccacagc tcctgggggt ttcattctgt tcttactgtt 360
 gtctggatta ggagggcgga gaggggtggac tcctgagac aagataagca ggtggagaca 420
 tagaagaggg agggacattt aacatagtaa cattttcaga ggtgacagag atgatacacg 480
 ggcagctgga mttttgtgaa ggacagagga gctggcagac ccacagggcc atacctttga 540
 gggacaggtg aatggctggg taccagagac aggactggtg gacagtcaag tacctcacta 600
 cgatgtgcca agagatyttg gatcctggga aatgtgtgga gaagaggatt tgacactccc 660
 ccccccaag gcccttcccc tttgctgaca gcattgctgt ggtcgtggcc tgttgcttg 720
 tcctctgtcc ctgggtgggg cacaccctcc tgtgctgtgc ttgccttggt catcaataaa 780
 cc 782

<210> 52
 <211> 1613
 <212> DNA
 <213> Eukaryote

<220>

<221> misc_feature
 <222> (1)...(1613)
 <223> r = G or A
 n = A,T,C or G

<400> 52

gcanttttggga	ggttattgctt	aaaaccaggn	taaggcactt	tgtcccacag	gaccagggaa	60
tcntaaangg	ggtgaaattg	ggncggggaa	ccccaggata	taatgcnact	tttgtaggg	120
ggagagttca	gctctaactg	gtagtagtgt	gaaagtaagc	accttgactt	caatttttggga	180
aagcacttgg	taaattggaga	gaacttttggga	gtttccctat	catctatatc	agtctttgaa	240
cacaccctca	agtcccagcc	tcaaggctca	ataaaggacc	acatagcagg	tctgaggctc	300
actgctctca	gcccttaaca	cagggcagtg	gagagcaggg	tgatcttccc	tctctggagc	360
ttctccttgg	ccttcttctc	cacttgggct	tctgctcagc	agcagatata	ttctgggttc	420
cataaggaat	ccagctgtcc	cagtggcttg	accctgtcaa	ggcaagatat	caactctgag	480
gatgaccag	tcatggagga	agagagtgtg	acaagatccg	cagtttgaag	caaaactgtg	540
tttggtcttt	tcaagaaaca	aatgggcaca	ttgagttctg	ttcagtgtca	gaggatatct	600
ttccctttgc	tcccagattt	ccagaaatgg	ataatgtttt	catttctgtg	ggaagggtca	660
agaaacataa	aattgctcaa	caatgcttgc	ttcccttgag	ggttggttgag	caaaggccga	720
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cagctctgtat	cttctaartt	aaacaggaac	tgggcttttg	cggcctattg	accagttta	900
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<210> 53

<211> 1669

<212> DNA

<213> Eukaryote

<400> 53

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<210> 54

<211> 1586

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1586)

<223> n = A,T,C or G

<400> 54

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gttgctgtcc	caagttcttc	agttacaacc	gagtacactt	actcttccaa	ctgtcctaag	360
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<210> 55

<211> 770

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(770)

<223> n = A,T,C or G

<400> 55

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<210> 56

<211> 983

<212> DNA

<213> Eukaryote

<400> 56

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<210> 57

<211> 1763

<212> DNA

<213> Eukaryote

<220>

<221> misc_feature

<222> (1)...(1763)

<223> y = C or T

n = A,T,C or G

<400> 57

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<210> 58

<211> 4634

<212> DNA

<213> Rattus norvegicus

<220>

<221> misc_feature

<222> (1)...(4634)

<223> r = G or A

y = C or T

m = A or C

k = G or T

s = G or C

w = A or T

n = A,T,C or G

<400> 58

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 actccaaact gaaattcagt ttggctttga gtatgtgcac acgtgggtggg ttcacctact 4500
 tcagtgttga ccaaaagttt atttttctag tgcatttttc taaatggtaa aaatatgtaa 4560
 ttttagtatg catgactggg tctccaaaat aaaaactgag tgtattgtga aaaaaaaaaa 4620
 aaaaaaaaaa aaaa 4634

<210> 59

<211> 1030

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)...(1030)

<400> 59

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Met Ser Glu Glu Ser Asp Ser Val Arg Thr Ser Pro Ser Val Ala Ser	
1 5 10 15	
ctc tcc gaa aat gag ctg cca ccg cct ccc ccg gaa cct ccc ggc tac	96
Leu Ser Glu Asn Glu Leu Pro Pro Pro Pro Glu Pro Pro Gly Tyr	
20 25 30	
gtg tgc tcg ctg aca gaa gac ttg gtc acc aag gcc agg gaa gag ctt	144
Val Cys Ser Leu Thr Glu Asp Leu Val Thr Lys Ala Arg Glu Glu Leu	
35 40 45	
cag gag aag ccc gag tgg aga ctc cgg gat gtg cag gcc ctt cga gac	192
Gln Glu Lys Pro Glu Trp Arg Leu Arg Asp Val Gln Ala Leu Arg Asp	
50 55 60	
atg gta cgg aag gag tac cca tac ctg agt aca tcg ctg gat gat gcc	240
Met Val Arg Lys Glu Tyr Pro Tyr Leu Ser Thr Ser Leu Asp Asp Ala	
65 70 75 80	
ttc ctg ttg cgc ttt ctg agg gcc cga aag ttt gat tat gac cgg gcc	288
Phe Leu Leu Arg Phe Leu Arg Ala Arg Lys Phe Asp Tyr Asp Arg Ala	
85 90 95	
ctg cag ctg ctg gtc aac tac cat ggc tgc agg cgg agc tgg cca gag	336
Leu Gln Leu Leu Val Asn Tyr His Gly Cys Arg Arg Ser Trp Pro Glu	
100 105 110	
gtc ttc agc aac ctg agg cca tca gcc ctg aaa gac gtt ctt aac tct	384
Val Phe Ser Asn Leu Arg Pro Ser Ala Leu Lys Asp Val Leu Asn Ser	
115 120 125	
gga ttc ctc aca gtg ctg ccc cac aca gac ccc agg ggc tgc cat gtc	432
Gly Phe Leu Thr Val Leu Pro His Thr Asp Pro Arg Gly Cys His Val	
130 135 140	
ctc tgc atc cga cca gac aga tgg ata ccg agc aac tac ccg atc acc	480
Leu Cys Ile Arg Pro Asp Arg Trp Ile Pro Ser Asn Tyr Pro Ile Thr	
145 150 155 160	
gag aac atc cgc gcc atc tac ttg acg tta gaa aaa ctc att cag tcc	528
Glu Asn Ile Arg Ala Ile Tyr Leu Thr Leu Glu Lys Leu Ile Gln Ser	
165 170 175	
gag gag acc cag gtg aac ggg gtt gta atc ctc gcc gac tac aag gga	576
Glu Glu Thr Gln Val Asn Gly Val Val Ile Leu Ala Asp Tyr Lys Gly	
180 185 190	
gtg agc tta tca aag gcg tct cac ttt ggc ccc ttt atc gcc aga aag	624
Val Ser Leu Ser Lys Ala Ser His Phe Gly Pro Phe Ile Ala Arg Lys	
195 200 205	
gtg att ggc atc ctt cag gat ggc ttc ccc att cgg ata aaa gca gtt	672
Val Ile Gly Ile Leu Gln Asp Gly Phe Pro Ile Arg Ile Lys Ala Val	

210	215	220	
cac ata gta aac gaa cct cgg ata ttt aag ggc att ttc gcc atc ata			720
His Ile Val Asn Glu Pro Arg Ile Phe Lys Gly Ile Phe Ala Ile Ile			
225	230	235	240
aaa cca ttt ctg aag gag aaa att gca aac agg ttc ttc ctc cat ggg			768
Lys Pro Phe Leu Lys Glu Lys Ile Ala Asn Arg Phe Phe Leu His Gly			
245	250		255
tct gac ctg agc tct ctg cac acg agc ctt cca agg aat atc ctc ccc			816
Ser Asp Leu Ser Ser Leu His Thr Ser Leu Pro Arg Asn Ile Leu Pro			
260	265		270
aaa gag tat ggg ggc acc gct ggg gag ctg gac act gcc agc tgg aac			864
Lys Glu Tyr Gly Gly Thr Ala Gly Glu Leu Asp Thr Ala Ser Trp Asn			
275	280		285
gcg gtg ctg ctg gcc tcg gag gat gat ttt gtg aaa gag ttc tgc cag			912
Ala Val Leu Leu Ala Ser Glu Asp Asp Phe Val Lys Glu Phe Cys Gln			
290	295	300	
cct gag tct ggc tgc gat ggt ctc ttg ggc cag ccc ctg ctg cct gag			960
Pro Glu Ser Gly Cys Asp Gly Leu Leu Gly Gln Pro Leu Leu Pro Glu			
305	310	315	320
ggg ctg atc tca gac gcg cag tgt gac gac tcc atg cga gcc atg aag			1008
Gly Leu Ile Ser Asp Ala Gln Cys Asp Asp Ser Met Arg Ala Met Lys			
325	330		335
tcc cag ctc tac tcc tgc tat t			1030
Ser Gln Leu Tyr Ser Cys Tyr			
340			

<210> 60

<211> 342

<212> PRT

<213> Rattus norvegicus

<400> 60

Ser Glu Glu Ser Asp Ser Val Arg Thr Ser Pro Ser Val Ala Ser Leu			
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Ser Glu Asn Glu Leu Pro Pro Pro Pro Pro Glu Pro Pro Gly Tyr Val			
20	25		30
Cys Ser Leu Thr Glu Asp Leu Val Thr Lys Ala Arg Glu Glu Leu Gln			
35	40		45
Glu Lys Pro Glu Trp Arg Leu Arg Asp Val Gln Ala Leu Arg Asp Met			
50	55	60	
Val Arg Lys Glu Tyr Pro Tyr Leu Ser Thr Ser Leu Asp Asp Ala Phe			
65	70	75	80
Leu Leu Arg Phe Leu Arg Ala Arg Lys Phe Asp Tyr Asp Arg Ala Leu			
85	90		95
Gln Leu Leu Val Asn Tyr His Gly Cys Arg Arg Ser Trp Pro Glu Val			
100	105		110
Phe Ser Asn Leu Arg Pro Ser Ala Leu Lys Asp Val Leu Asn Ser Gly			
115	120		125
Phe Leu Thr Val Leu Pro His Thr Asp Pro Arg Gly Cys His Val Leu			
130	135	140	
Cys Ile Arg Pro Asp Arg Trp Ile Pro Ser Asn Tyr Pro Ile Thr Glu			

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<220>  
<221> CDS  
<222> (1) ... (1029)
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1				5					10					15		
ctc	tct	gaa	aat	gag	ctg	cca	cca	cca	cct	gag	cct	ccg	ggc	tat	gtg	96
Leu	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Pro	Glu	Pro	Pro	Gly	Tyr	Val	
			20					25					30			
tgc	tca	ctg	aca	gaa	gac	ctg	gtc	acc	aaa	gcc	cgg	gaa	gag	ctg	cag	144
Cys	Ser	Leu	Thr	Glu	Asp	Leu	Val	Thr	Lys	Ala	Arg	Glu	Glu	Leu	Gln	
		35					40					45				
gaa	aag	ccg	gaa	tgg	aga	ctt	cga	gat	gtg	cag	gcc	ctt	cgt	gac	atg	192
Glu	Lys	Pro	Glu	Trp	Arg	Leu	Arg	Asp	Val	Gln	Ala	Leu	Arg	Asp	Met	
	50					55					60					
gtg	cgg	aag	gag	tac	ccc	aac	ctg	agc	aca	tcc	ctc	gac	gat	gcc	ttc	240
Val	Arg	Lys	Glu	Tyr	Pro	Asn	Leu	Ser	Thr	Ser	Leu	Asp	Asp	Ala	Phe	
65					70					75					80	
ctg	ctg	cgc	ttc	ctc	cga	gcc	cgc	aag	ttt	gat	tac	gac	cgg	gcc	ctg	288
Leu	Leu	Arg	Phe	Leu	Arg	Ala	Arg	Lys	Phe	Asp	Tyr	Asp	Arg	Ala	Leu	
				85					90					95		

cag ctc ctc gtc aac tac cac agc tgt aga aga agc tgg ccc gaa gtc	336
Gln Leu Leu Val Asn Tyr His Ser Cys Arg Arg Ser Trp Pro Glu Val	
100 105 110	
ttc aat aac ttg aag cca tca gcc tta aaa gat gtc ctt gct tcc ggg	384
Phe Asn Asn Leu Lys Pro Ser Ala Leu Lys Asp Val Leu Ala Ser Gly	
115 120 125	
ttc ctc acc gtg ctg ccc cac act gac ccc agg ggc tgc cat gtc gtc	432
Phe Leu Thr Val Leu Pro His Thr Asp Pro Arg Gly Cys His Val Val	
130 135 140	
tgc atc cgc cca gac aga tgg ata cca agc aac tat cca att act gaa	480
Cys Ile Arg Pro Asp Arg Trp Ile Pro Ser Asn Tyr Pro Ile Thr Glu	
145 150 155 160	
aac atc cga gcc ata tac ttg acc tta gaa aaa ctc att cag tct gaa	528
Asn Ile Arg Ala Ile Tyr Leu Thr Leu Glu Lys Leu Ile Gln Ser Glu	
165 170 175	
gaa acc cag gtg aat gga att gta att ctt gca gac tac aaa gga gtg	576
Glu Thr Gln Val Asn Gly Ile Val Ile Leu Ala Asp Tyr Lys Gly Val	
180 185 190	
agt tta tca aaa gca tct cac ttt ggc cct ttt ata gcc aaa aag gtg	624
Ser Leu Ser Lys Ala Ser His Phe Gly Pro Phe Ile Ala Lys Lys Val	
195 200 205	
att ggc atc ctc cag gat ggt ttc ccc att cgg ata aaa gca gtc cat	672
Ile Gly Ile Leu Gln Asp Gly Phe Pro Ile Arg Ile Lys Ala Val His	
210 215 220	
gtg gtg aat gaa cct cga ata ttt aaa ggc att ttt gcc atc ata aaa	720
Val Val Asn Glu Pro Arg Ile Phe Lys Gly Ile Phe Ala Ile Ile Lys	
225 230 235 240	
cca ttt cta aag gag aaa ata gca aac aga ttc ttc ctc cat ggg tct	768
Pro Phe Leu Lys Glu Lys Ile Ala Asn Arg Phe Phe Leu His Gly Ser	
245 250 255	
gac ttg aac tct ctc cac aca aac ctt cca aga agc atc ctc ccc aag	816
Asp Leu Asn Ser Leu His Thr Asn Leu Pro Arg Ser Ile Leu Pro Lys	
260 265 270	
gag tat ggg ggc acg gct ggg gag ctg gac act gcc acc tgg aac gca	864
Glu Tyr Gly Gly Thr Ala Gly Glu Leu Asp Thr Ala Thr Trp Asn Ala	
275 280 285	
gta ctg ctg gct tca gaa gac gat ttt gtg aaa gag ttc tgc caa cct	912
Val Leu Leu Ala Ser Glu Asp Asp Phe Val Lys Glu Phe Cys Gln Pro	
290 295 300	
gtt cct gcc tgt gac agc atc ctg ggc cag acg ctg ctg ccc gag ggc	960
Val Pro Ala Cys Asp Ser Ile Leu Gly Gln Thr Leu Leu Pro Glu Gly	
305 310 315 320	
ctg acc tca gat gca cag tgt gac gac tcc ttg cga gct gtg aag tca	1008
Leu Thr Ser Asp Ala Gln Cys Asp Asp Ser Leu Arg Ala Val Lys Ser	
325 330 335	

cag ctg tac tcc tgc tac tag
Gln Leu Tyr Ser Cys Tyr *
340

<210> 62
<211> 341
<212> PRT
<213> Rattus norvegicus

<220>
<221> VARIANT
<222> (1)...(341)
<223> Xaa = Any Amino Acid

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Leu Ser Glu Asn Glu Leu Pro Pro Pro Pro Pro Glu Pro Pro Xaa Tyr
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Val Cys Ser Leu Thr Glu Asp Leu Val Thr Lys Ala Arg Glu Glu Leu
35 40 45
Gln Glu Lys Pro Glu Trp Arg Leu Arg Asp Val Gln Ala Leu Arg Asp
50 55 60
Met Val Arg Lys Glu Tyr Pro Tyr Leu Ser Thr Ser Leu Asp Asp Ala
65 70 75 80
Phe Leu Leu Arg Phe Leu Arg Ala Arg Lys Phe Asp Tyr Asp Arg Ala
85 90 95
Leu Gln Leu Leu Val Asn Tyr His Gly Cys Arg Arg Ser Trp Pro Glu
100 105 110
Val Phe Ser Asn Leu Arg Pro Ser Ala Leu Lys Asp Val Leu Asn Ser
115 120 125
Gly Phe Leu Thr Val Leu Pro His Thr Asp Pro Arg Gly Cys His Val
130 135 140
Leu Cys Ile Arg Pro Asp Arg Trp Ile Pro Ser Asn Tyr Pro Ile Thr
145 150 155 160
Glu Asn Ile Arg Ala Ile Tyr Leu Thr Leu Glu Lys Leu Ile Gln Ser
165 170 175
Glu Glu Thr Gln Val Asn Gly Val Val Ile Leu Ala Asp Tyr Lys Gly
180 185 190
Val Ser Leu Ser Lys Ala Ser His Phe Gly Pro Phe Ile Ala Arg Lys
195 200 205
Val Ile Gly Ile Leu Gln Asp Gly Phe Pro Ile Arg Ile Lys Ala Val
210 215 220
His Ile Val Asn Glu Pro Arg Ile Phe Lys Gly Ile Phe Ala Ile Ile
225 230 235 240
Lys Pro Phe Leu Lys Glu Lys Ile Ala Asn Arg Phe Phe Leu His Gly
245 250 255
Ser Asp Leu Ser Ser Leu His Thr Ser Leu Pro Arg Asn Ile Leu Pro
260 265 270
Lys Glu Tyr Gly Gly Thr Ala Gly Glu Leu Asp Thr Ala Ser Trp Asn
275 280 285
Ala Val Leu Leu Ala Ser Glu Asp Asp Phe Val Lys Glu Phe Cys Gln
290 295 300
Pro Glu Ser Gly Cys Asp Gly Leu Leu Gly Gln Pro Leu Leu Pro Glu
305 310 315 320
Gly Leu Ile Ser Asp Ala Gln Cys Asp Asp Ser Met Arg Ala Met Lys
325 330 335
Ser Gln Leu Tyr Ser
340

<210> 63
 <211> 342
 <212> PRT
 <213> Homo sapiens

<400> 63

Met Ser Glu Glu Arg Asp Ser Leu Arg Thr Ser Pro Ser Val Ala Ser
 1 5 10 15
 Leu Ser Glu Asn Glu Leu Pro Pro Pro Glu Pro Pro Gly Tyr Val
 20 25 30
 Cys Ser Leu Thr Glu Asp Leu Val Thr Lys Ala Arg Glu Glu Leu Gln
 35 40 45
 Glu Lys Pro Glu Trp Arg Leu Arg Asp Val Gln Ala Leu Arg Asp Met
 50 55 60
 Val Arg Lys Glu Tyr Pro Asn Leu Ser Thr Ser Leu Asp Asp Ala Phe
 65 70 75 80
 Leu Leu Arg Phe Leu Arg Ala Arg Lys Phe Asp Tyr Asp Arg Ala Leu
 85 90 95
 Gln Leu Leu Val Asn Tyr His Ser Cys Arg Arg Ser Trp Pro Glu Val
 100 105 110
 Phe Asn Asn Leu Lys Pro Ser Ala Leu Lys Asp Val Leu Ala Ser Gly
 115 120 125
 Phe Leu Thr Val Leu Pro His Thr Asp Pro Arg Gly Cys His Val Val
 130 135 140
 Cys Ile Arg Pro Asp Arg Trp Ile Pro Ser Asn Tyr Pro Ile Thr Glu
 145 150 155 160
 Asn Ile Arg Ala Ile Tyr Leu Thr Leu Glu Lys Leu Ile Gln Ser Glu
 165 170 175
 Glu Thr Gln Val Asn Gly Ile Val Ile Leu Ala Asp Tyr Lys Gly Val
 180 185 190
 Ser Leu Ser Lys Ala Ser His Phe Gly Pro Phe Ile Ala Lys Lys Val
 195 200 205
 Ile Gly Ile Leu Gln Asp Gly Phe Pro Ile Arg Ile Lys Ala Val His
 210 215 220
 Val Val Asn Glu Pro Arg Ile Phe Lys Gly Ile Phe Ala Ile Ile Lys
 225 230 235 240
 Pro Phe Leu Lys Glu Lys Ile Ala Asn Arg Phe Phe Leu His Gly Ser
 245 250 255
 Asp Leu Asn Ser Leu His Thr Asn Leu Pro Arg Ser Ile Leu Pro Lys
 260 265 270
 Glu Tyr Gly Gly Thr Ala Gly Glu Leu Asp Thr Ala Thr Trp Asn Ala
 275 280 285
 Val Leu Leu Ala Ser Glu Asp Asp Phe Val Lys Glu Phe Cys Gln Pro
 290 295 300
 Val Pro Ala Cys Asp Ser Ile Leu Gly Gln Thr Leu Leu Pro Glu Gly
 305 310 315 320
 Leu Thr Ser Asp Ala Gln Cys Asp Asp Ser Leu Arg Ala Val Lys Ser
 325 330 335
 Gln Leu Tyr Ser Cys Tyr
 340